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 PR 28-OCT-1999; 99US-0161993P.
 PR 29-OCT-1999; 99US-0162142P.

Query Match Similarity 99.7%; Score 1579; DB 3; Length 308;
 Best Local Similarity 99.7%; Pred. No. 5.1e-166;
 Matches 307; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

SQ Sequence 308 AA;
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 Db 1 MAEENLELLSLLCETESNYDDEGMIVDEPIEISIPOMGFSQSEEEITIMEMYKEKQHILPS 60
 Qy 61 DDYIKRURSGDLDLNVGRDAINWIKVACEVHQGPLOCFLAMNYLDRFLSPHGKG 120
 Db 61 DDYIKRURSGDLDLNVGRDAINWIKVACEVHQGPLOCFLAMNYLDRFLSPHGKG 120
 Qy 121 WIQLLAVACSLAAKLEETEVPMELIDIQGDQFVFEAKSYORMELIVNLKWKRLRAI 180
 Db 121 WIQLLAVACSLAAKLEETEVPMELIDIQGDQFVFEAKSYORMELIVNLKWKRLRAI 180
 Qy 181 TPCSYIRXFLRKMSKCDOPSNLTLISRSILQVIASTTKGIDLEFRPSFAAVALSVSGE 240
 Db 181 TPCSYIRXFLRKMSKCDOPSNLTLISRSILQVIASTTKGIDLEFRPSFAAVALSVSGE 240
 Qy 241 LQRVFHDNSFSPLSFSLQQERYKKIGMIESGDSLCSQTENGVLEVSACCFSFKTHDS 300
 Db 241 LQRVFHDNSFSPLSFSLQQERYKKIGMIESGDSLCSQTENGVLEVSACCFSFKTHDS 300
 Qy 301 SSSYTHLS 308
 Db 301 SSSYTHLS 308

RESULT 2
 AAY14071 standard; protein; 308 AA.
 ID AAY14071
 XX AC AAY14071;
 XX DT 16-JUL-1999 (First entry)
 XX DE Mitogenic cyclin CYCD4 protein sequence.
 XX KW Mitogenic cyclin; CYCD4; modulator; plant cell cycle; growth inhibitor;
 plant cell division; cell growth regulator; cell proliferation;
 growth regulator; herbicide; cell division progression.
 XX OS Arabidopsis thaliana.
 PN WO9922002-A1.
 XX PD 06-MAY-1999.
 XX PF 23-OCT-1998; 98WO-EP006749.
 XX PR 24-OCT-1997; 97EP-00203303.
 XX PA (CROP-) CROBDESIGN NV.
 XX PI Inze D, De Veylder L, De Almeide J;
 XX DR WPI: 1999-312566/26.
 N-PSDB; AAX36897.
 XX PT DNA sequence encoding a mitogenic cyclin.
 XX PS Claim 1; Page 47-49; 57PP; English.
 XX

CC This sequence is the mitogenic cyclin, CYCD4 of the invention. The DNA sequence, vectors containing it, protein encoded by it, or antibodies
 CC recognising the protein can be used for modulating plant cell cycle,
 CC plant cell division and/or growth, for influencing the activity of
 CC mitogenic cyclin in a plant cell, as positive or negative regulator of
 CC cell proliferation, for modifying the growth inhibition caused by
 CC environmental stress conditions, or for use in a screening method for the
 CC identification of inhibitors or activators of cell cycle proteins. A
 CC compound which is an activator or inhibitor of the mitogenic cyclin can
 CC be used as a growth regulator and/or herbicide. The proteins can also be
 CC used to influence cell division progression in yeast, mammals and insects

CC Sequence 308 AA;
 Query Match 99.4%; Score 1573; DB 2; Length 308;
 Best Local Similarity 99.7%; Pred. No. 2.4e-165;
 Matches 307; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MAEENLELLSLLCETESNYDDEGMIVDEPIEISIPOMGFSQSEEEITIMEMYKEKQHILPS 60
 Db 1 MAEENLELLSLLCETESNYDDEGMIVDEPIEISIPOMGFSQSEEEITIMEMYKEKQHILPS 60
 Qy 61 DDYIKRURSGDLDLNVGRDAINWIKVACEVHQGPLOCFLAMNYLDRFLSPHGKG 120
 Db 61 DDYIKRURSGDLDLNVGRDAINWIKVACEVHQGPLOCFLAMNYLDRFLSPHGKG 120
 Qy 121 WIQLLAVACSLAAKLEETEVPMELIDIQGDQFVFEAKSYORMELIVNLKWKRLRAI 180
 Db 121 WIQLLAVACSLAAKLEETEVPMELIDIQGDQFVFEAKSYORMELIVNLKWKRLRAI 180
 Qy 181 TPCSYIRXFLRKMSKCDOPSNLTLISRSILQVIASTTKGIDLEFRPSFAAVALSVSGE 240
 Db 181 TPCSYIRXFLRKMSKCDOPSNLTLISRSILQVIASTTKGIDLEFRPSFAAVALSVSGE 240
 Qy 241 LQRVFHDNSFSPLSFSLQQERYKKIGMIESGDSLCSQTENGVLEVSACCFSFKTHDS 300
 Db 241 LQRVFHDNSFSPLSFSLQQERYKKIGMIESGDSLCSQTENGVLEVSACCFSFKTHDS 300
 Qy 301 SSSYTHLS 308
 Db 301 SSSYTHLS 308

RESULT 3
 AAC23337
 ID AAC23337 standard; protein; 308 AA.
 XX AC AAC23337;
 XX DT 17-OCT-2000 (first entry)
 XX DE Arabidopsis thaliana protein fragment SEQ ID NO: 26608.
 KW Protein identification; signal transduction pathway; metabolic pathway;
 KW hybridisation assay; genetic mapping; gene expression; promoter;
 KW termination sequence.
 XX OS Arabidopsis thaliana.
 XX PN EP1033405-A2.
 XX PD 06-SEP-2000.
 XX PP 25-FEB-2000; 2000EP-00301439.
 XX PR 25-FEB-1999; 99US-0121825P.
 PR 05-MAR-1999; 99US-0123180P.
 PR 09-MAR-1999; 99US-0123548P.
 PR 23-MAR-1999; 99US-0125788P.
 PR 25-MAR-1999; 99US-0126264P.
 PR 29-MAR-1999; 99US-0126785P.
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PR	08-APR-1999;	99US-0128714P.	PR	19-JUL-1999;	99US-0144333P.
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PR	21-APR-1999;	99US-0131044P.	PR	20-JUL-1999;	99US-0144332P.
PR	23-APR-1999;	99US-0130510P.	PR	20-JUL-1999;	99US-0144632P.
PR	23-APR-1999;	99US-0130891P.	PR	20-JUL-1999;	99US-0144884P.
PR	28-APR-1999;	99US-0131449P.	PR	21-JUL-1999;	99US-0144814P.
PR	30-APR-1999;	99US-0132048P.	PR	21-JUL-1999;	99US-0145086P.
PR	30-APR-1999;	99US-0132407P.	PR	21-JUL-1999;	99US-0145088P.
PR	04-MAY-1999;	99US-0132484P.	PR	22-JUL-1999;	99US-0145085P.
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PR	07-MAY-1999;	99US-0132487P.	PR	22-JUL-1999;	99US-0145192P.
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PR			PR	18-JUN-1999;	99US-0139458P.
PR			PR	18-JUN-1999;	99US-0139459P.
PR			PR	21-JUN-1999;	99US-0139817P.
DE			PR	22-JUN-1999;	99US-0139899P.
XX			PR	23-JUN-1999;	99US-0140353P.
AC	AAG47104;	Arabidopsis thaliana protein fragment SEQ ID NO: 59334.	PR	23-JUN-1999;	99US-0139462P.
XX		Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.	PR	24-JUN-1999;	99US-0140354P.
KW			PR	28-JUN-1999;	99US-0140695P.
KW			PR	29-JUN-1999;	99US-0140991P.
OS		Arabidopsis thaliana.	PR	30-JUL-1999;	99US-0141287P.
XX			PR	01-JUL-1999;	99US-0141842P.
PN	EPI33405-A2.		PR	01-JUL-1999;	99US-0142154P.

RESULT 4

AAG47104
ID AAG47104 standard; protein; 28 AA.DE Arabidopsis thaliana protein fragment SEQ ID NO: 59334.
XX Protein identification; signal transduction pathway; metabolic pathway;
AC hybridisation assay; genetic mapping; gene expression control; promoter;
XX termination sequence.

KW Arabidopsis thaliana.

XX EPI33405-A2.

PR 02-JUL-1999; 99US-0142055P.
 PR 06-JUL-1999; 99US-0142300P.
 PR 08-JUL-1999; 99US-0142803P.
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 PR 02-AUG-1999; 99US-0146388P.
 PR 03-AUG-1999; 99US-0146389P.
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 PR 10-AUG-1999; 99US-0148171P.
 PR 11-AUG-1999; 99US-0148319P.
 PR 12-AUG-1999; 99US-0148341P.
 PR 13-AUG-1999; 99US-0148665P.
 PR 13-AUG-1999; 99US-0148829P.
 PR 16-AUG-1999; 99US-0149468P.
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 PR 18-AUG-1999; 99US-0149840P.
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 PR 31-AUG-1999; 99US-0151438P.
 PR 01-SEP-1999; 99US-0150566P.
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 PR 09-SEP-1999; 99US-0151307P.
 PR 13-SEP-1999; 99US-0153758P.
 PR 15-SEP-1999; 99US-0154018P.
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PR 22-SEP-1999; 99US-0155139P.
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 PR 24-SEP-1999; 99US-0155659P.
 PR 28-SEP-1999; 99US-0156458P.
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 PR 04-OCT-1999; 99US-0157117P.
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 PR 25-OCT-1999; 99US-0161414P.
 PR 25-OCT-1999; 99US-0161405P.
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 PR 26-OCT-1999; 99US-0161360P.
 PR 26-OCT-1999; 99US-0161361P.
 PR 28-OCT-1999; 99US-0161920P.
 PR 28-OCT-1999; 99US-0161920P.
 PR 28-OCT-1999; 99US-0161992P.
 PR 29-OCT-1999; 99US-0161993P.
 PR 29-OCT-1999; 99US-016214P.

Query Match 93.1%; Score 1473; DB 3; Length 287;
 Best Local Similarity 93.7%; Pred. No. 2, 6e-164;
 Matches 286; Conservative 0; Mismatches 1; Indexes 0; Gaps 0;

Qy 22 MIVDTEPIISIOPGMGEPOSESEITIMEMVEKEKOHLPSSDDYIKRRLRSGLDLINVGGRDA 81
 Db 1 MIVDTEPIISIOPGMGEPOSESEBIIIMMVEKEKQHLESDDYIKRRLRSGLDLINVGGRDA 60

Qy 82 LNNWIKACEVHQGPCLFLANNYLDRFLSYHDLPSGKGWLQLLAVALSAAKIEETE 141
 Db 61 LNNWIKACEVHQGPCLFLANNYLDRFLSYHDLPSGKGWLQLLAVALSAAKIEETE 120

Qy 202 NTLISSLQVIATSTTKGIDFLEFRPSEAAAVALSVSGELQRVHFNDNSFSPLSFLLKKE 261
 Db 181 NTLISSLQVIATSTTKGIDFLEFRPSEAAAVALSVSGELQRVHFNDNSFSPLSFLLKKE 240

Qy 142 VPMELDLQVGDPOFVPEAKSVORMELLYNKLKWRRLATPCSYIRYFLRKMSKCDQEPS 201
 Db 121 VPMELDLQVGDPOFVPEAKSVORMELLYNKLKWRRLATPCSYIRYFLRKMSKCDQEPS 180

Qy 262 RVKCGIEMEESDGSDLCQSQTPNGLEVSAACFCSPKTHDSSSSYTHLS 308
 Db 241 RVKCGIEMEESDGSDLCQSQTPNGLEVSAACFCSPKTHDSSSSYTHLS 287

RESULT 5
 ID AAG23338 Standard, protein; 287 AA.
 XX AC
 XX DT 17-OCT-2000 (first entry)
 XX

Arabidopsis thaliana protein fragment SEQ ID NO: 26609.

XX DE Protein identification; signal transduction pathway; metabolic pathway;
 KW hybridisation assay; genetic mapping; gene expression control; promoter;
 KW termination sequence.

Arabidopsis thaliana.

XX DE EP1033405-A2.

PN PR 05-SEP-2000.

XX PD 25-FEB-2000; 20000BP-00301439.

XX PR 25-FEB-1999;

PR 05-MAR-1999;

PR 09-MAR-1999;

PR 25-MAR-1999;

PR 29-MAR-1999;

PR 01-APR-1999;

PR 05-APR-1999;

PR 08-APR-1999;

PR 19-APR-1999;

PR 21-APR-1999;

PR 23-APR-1999;

PR 28-APR-1999;

PR 30-APR-1999;

PR 04-MAY-1999;

PR 06-MAY-1999;

PR 06-MAY-1999;

PR 11-MAY-1999;

PR 14-MAY-1999;

PR 14-MAY-1999;

PR 14-MAY-1999;

PR 19-MAY-1999;

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PR 24-MAY-1999;

PR 25-MAY-1999;

PR 27-MAY-1999;

PR 28-MAY-1999;

PR 01-JUN-1999;

PR 03-JUN-1999;

PR 04-JUN-1999;

PR 07-JUN-1999;

PR 08-JUN-1999;

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PR 18-JUN-1999;

PR 21-JUN-1999;

PR 25-AUG-1999;

PR 26-AUG-1999;

PR 27-AUG-1999;

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 99US-0142055P.
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PR	30-AUG-1999;	99US-0151303P.
PR	31-AUG-1999;	99US-0151438P.
PR	01-SEP-1999;	99US-0151930P.
PR	07-SEP-1999;	99US-0152263P.
PR	10-SEP-1999;	99US-0153070P.
PR	13-SEP-1999;	99US-0153758P.
PR	15-SEP-1999;	99US-0154018P.
PR	16-SEP-1999;	99US-0154039P.
PR	20-SEP-1999;	99US-0154779P.
PR	22-SEP-1999;	99US-0155139P.
PR	23-SEP-1999;	99US-0155486P.
PR	24-SEP-1999;	99US-0155659P.
PR	28-SEP-1999;	99US-0156589P.
PR	29-SEP-1999;	99US-0156596P.
PR	04-OCT-1999;	99US-0157117P.
PR	05-OCT-1999;	99US-0157153P.
PR	06-OCT-1999;	99US-0157865P.
PR	07-OCT-1999;	99US-0158029P.
PR	08-OCT-1999;	99US-0158232P.
PR	12-OCT-1999;	99US-0158369P.
PR	13-OCT-1999;	99US-0159233P.
PR	13-OCT-1999;	99US-0159294P.
PR	13-OCT-1999;	99US-0159255P.
PR	14-OCT-1999;	99US-0159310P.
PR	14-OCT-1999;	99US-0159331P.
PR	14-OCT-1999;	99US-0159631P.
PR	14-OCT-1999;	99US-0159638P.
PR	18-OCT-1999;	99US-0159549P.
PR	21-OCT-1999;	99US-0160741P.
PR	21-OCT-1999;	99US-0160767P.
PR	21-OCT-1999;	99US-0160788P.
PR	21-OCT-1999;	99US-0160770P.
PR	21-OCT-1999;	99US-0160814P.
PR	21-OCT-1999;	99US-0160815P.
PR	22-OCT-1999;	99US-0160980P.
PR	22-OCT-1999;	99US-0160981P.
PR	22-OCT-1999;	99US-0160989P.
PR	25-OCT-1999;	99US-0161404P.
PR	25-OCT-1999;	99US-0161405P.
PR	25-OCT-1999;	99US-0161406P.
PR	26-OCT-1999;	99US-0161359P.
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PR	26-OCT-1999;	99US-0161361P.
PR	28-OCT-1999;	99US-0161920P.
PR	28-OCT-1999;	99US-0161993P.
PR	28-OCT-1999;	99US-0162142P.
PR	29-OCT-1999;	99US-0162142P.
QY	22 MIVDTEPIEISITQMGFQSSESBIIIMMEMVEKEKQHLPSSDDYTKRSGDLDLNVGRDA	81
Db	1 MIVDTEPIEISITQMGFQSSESBIIIMMEMVEKEKQHLPSSDDYTKRSGDLDLNVGRDA	60
QY	142 VPMJLIDQGDQFVFEARKSFORMELLYNKLKWRLRAITPCSYIYFLRKISKCDQPS	201
Db	121 VPMJLIDQGDQFVFEARKSFORMELLYNKLKWRLRAITPCSYIYFLRKISKCDQPS	180
QY	82 LNWTKACEVHQFGPLCFLAMNNYLDRETSVHDLPSGKGWILQLLAVACLSAAKTEETE	141
Db	61 LNWTKACEVHQFGPLCFLAMNNYLDRETSVHDLPSGKGWILQLLAVACLSAAKTEETE	120
QY	226 NTLISRSLQVIASTTKGIIDFLEFRPSEAAAVAVSVQRMLLQVYRFLRKISKCDQPS	180
Db	202 NTLISRSLQVIASTTKGIIDFLEFRPSEAAVAVSVQRMLLQVYRFLRKISKCDQPS	261
QY	181 NTLISRSLQVIASTTKGIIDFLEFRPSEAAVAVSVQRMLLQVYRFLRKISKCDQPS	240
Db	126 RVKKIGEMTESDGDLCSFTPQNGLEVSSACCFSKTHDSSSSYTHLS	308
QY	262 RVKKIGEMTESDGDLCSFTPQNGLEVSSACCFSKTHDSSSSYTHLS	287
Db	241 RVKKIGEMTESDGDLCSFTPQNGLEVSSACCFSKTHDSSSSYTHLS	287

Query Match Score 1459; DB 3; Length 287;
Best Local Similarity 99.0%; Pred: No 9; 4e-13; Indels 0; Gaps 0;

Matches 284; Conservative 1; Mismatches 2; Deletions 0; Insertions 0;

PR 19-MAY-1999; 99US-013441P.

PR 20-MAY-1999; 99US-013524P.

PR 21-MAY-1999; 99US-013553P.

PR 24-MAY-1999; 99US-013529P.

PR 25-MAY-1999; 99US-013602P.

PR 08-JUN-1999; 99US-0136792P.

PR 28-MAY-1999; 99US-0136782P.

PR 01-JUN-1999; 99US-013722P.

PR 03-JUN-1999; 99US-013758P.

PR 04-JUN-1999; 99US-0137502P.

PR 07-JUN-1999; 99US-0137724P.

PR 16-JUN-1999; 99US-013945P.

PR 17-JUN-1999; 99US-0139492P.

PR 18-JUN-1999; 99US-013944P.

PR 19-JUN-1999; 99US-013945P.

PR 18-JUN-1999; 99US-013945P.

PR 18-JUN-1999; 99US-013945T.

RESULT 6
Arabidopsis thaliana protein fragment SEQ ID NO: 59335.
Arabidopsis thaliana protein fragment standard; protein; 273 AA.
ID AAG47105
XX XX
AC AAG47105;
XX DT 18-OCT-2000 (first entry)
XX DE Arabidopsis thaliana protein fragment SEQ ID NO: 59335.
XX KW Protein identification; signal transduction pathway; metabolic pathway;
hybridisation assay; genetic mapping; gene expression control; promoter;
termination sequence.
XX OS Arabidopsis thaliana.
XX PN EP1033405-A2.
XX PD 06-SEP-2000.
XX PR 25-FEB-2000; 20000BP-00301439.

PR 18-JUN-1999; 99US-0139458P.
 PR 18-JUN-1999; 99US-0139459P.
 PR 18-JUN-1999; 99US-0139460P.
 PR 18-JUN-1999; 99US-0139461P.
 PR 18-JUN-1999; 99US-0139462P.
 PR 18-JUN-1999; 99US-0139463P.
 PR 18-JUN-1999; 99US-0139750P.
 PR 18-JUN-1999; 99US-0139763P.
 PR 21-JUN-1999; 99US-0139817P.
 PR 22-JUN-1999; 99US-0139839P.
 PR 23-JUN-1999; 99US-0140353P.
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 PR 28-JUN-1999; 99US-0140635P.
 PR 29-JUN-1999; 99US-0140911P.
 PR 30-JUN-1999; 99US-0141287P.
 PR 01-JUL-1999; 99US-0141842P.
 PR 02-JUL-1999; 99US-0142154P.
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 PR 20-JUL-1999; 99US-0144332P.
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 PR 22-JUL-1999; 99US-0145085P.
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 PR 04-AUG-1999; 99US-0147204P.
 PR 04-AUG-1999; 99US-0147302P.
 PR 05-AUG-1999; 99US-0147192P.
 PR 05-AUG-1999; 99US-0147260P.
 PR 06-AUG-1999; 99US-0147030P.
 PR 09-AUG-1999; 99US-0147492P.
 PR 09-AUG-1999; 99US-0147935P.
 PR 10-AUG-1999; 99US-0148171P.
 PR 11-AUG-1999; 99US-0148310P.
 PR 12-AUG-1999; 99US-0148341P.
 PR 13-AUG-1999; 99US-0148565P.
 PR 16-AUG-1999; 99US-0149368P.
 PR 17-AUG-1999; 99US-0149175P.
 PR 18-AUG-1999; 99US-0149422P.
 PR 20-AUG-1999; 99US-0149722P.

Query Match 88.7%; Score 1404; DB 3; Length 273;

Best Local Similarity 99.6%; Pred. No. 1..1e-146; Matches 1; Mismatches 0; Indels 0; Gaps 0;

36 MGFSOSSESEEITMENYVEKEROLHPLSPDDYIKRLRGSGDLDLNYGRDRDLNWIKACEVHOFG 95
 1 MGFSQSSESEEITMENYVEKEROLHPLSPDDYIKRLRGSGDLDLNYGRDRDLNWIKACEVHOFG 6096 PLCPCLAMNYLDREISYHDLSGKGHLLOLLAVACSLAAKIEETEYPMILQDLPQF 155
 61 PLCPCLAMNYLDREISYHDLSGKGHLLOLLAVACSLAAKIEETEYPMILQDLPQF 120QY 156 VPEAKSYQRMEILVNLKWLWLRATTPCSYTRYFLXMSKCDQEPTNTLRSLOVIAST 215
 121 VPEAKSYQRMEILVNLKWLWLRATTPCSYTRYFLXMSKCDQEPTNTLRSLOVIAST 180

Qy	216	TKGIDFILEFRPSEAAAVAVLSGELQRVHFDSSESPFLSLLQKERVKKIGEMMESDGs	275
Db	181	TKGIDFILEFRPSEAAAVAVLSGELQRVHFDSSESPFLSLLQKERVKKIGEMMESDGs	240
Qy	276	DLCSQTPGVLEVSACCSFKTHDSSSSYTHLS	308
Db	241	DLCSQTPGVLEVSACCFSFKTHDSSSSYTHLS	273
RESULT 7			
	AAG23339	AAG23339 standard; protein; 273 AA.	
ID	AAG23339		
XX			
AC	AAG23339;		
XX			
DT	17-OCT-2000	(first entry)	
XX			
DE		Arabidopsis thaliana protein fragment SEQ ID NO: 26610.	
XX			
KW		Protein identification; signal transduction pathway; metabolic pathway;	
KW		hybridisation assay; genetic mapping; gene expression control; promoter;	
KW		termination sequence.	
XX			
OS		Arabidopsis thaliana.	
XX			
PN	EP1033405-A2.		
XX			
PD	06-SEP-2000.		
XX			
PF	25-FEB-2000;	20000EP-00301439.	
XX			
PR	25-FEB-1999;	99US-0121825P.	
PR	05-MAR-1999;	99US-012180P.	
PR	03-MAR-1999;	99US-0125548P.	
PR	23-MAR-1999;	99US-0125188P.	
PR	25-MAR-1999;	99US-0126264P.	
PR	29-MAR-1999;	99US-0126785P.	
PR	01-APR-1999;	99US-01267462P.	
PR	06-APR-1999;	99US-0128234P.	
PR	08-APR-1999;	99US-0128214P.	
PR	16-APR-1999;	99US-0129445P.	
PR	19-APR-1999;	99US-0130077P.	
PR	21-APR-1999;	99US-0130449P.	
PR	23-APR-1999;	99US-0130510P.	
PR	23-APR-1999;	99US-0130891P.	
PR	28-APR-1999;	99US-0131449P.	
PR	30-APR-1999;	99US-0132048P.	
PR	04-MAY-1999;	99US-0132407P.	
PR	05-MAY-1999;	99US-0132444P.	
PR	06-MAY-1999;	99US-0132455P.	
PR	06-MAY-1999;	99US-0132486P.	
PR	07-MAY-1999;	99US-0132487P.	
PR	11-MAY-1999;	99US-0132863P.	
PR	14-MAY-1999;	99US-0134256P.	
PR	14-MAY-1999;	99US-0134218P.	
PR	14-MAY-1999;	99US-0134219P.	
PR	14-MAY-1999;	99US-0134221P.	
PR	14-MAY-1999;	99US-0134370P.	
PR	18-MAY-1999;	99US-0134768P.	
PR	19-MAY-1999;	99US-0134941P.	
PR	20-MAY-1999;	99US-0135124P.	
PR	21-MAY-1999;	99US-0135353P.	
PR	24-MAY-1999;	99US-0135629P.	
PR	25-MAY-1999;	99US-0136021P.	
PR	27-MAY-1999;	99US-0136392P.	
PR	28-MAY-1999;	99US-0136782P.	
PR	01-JUN-1999;	99US-0137222P.	
PR	03-JUN-1999;	99US-0137528P.	
PR	04-JUN-1999;	99US-0137502P.	
PR	07-JUN-1999;	99US-0137724P.	
PR	10-JUN-1999;	99US-0138094P.	

PR	10-AUG-1999;	99US-0148171P.	1 MGFSQSESEIIMVKEKQHLPSSDDYIKRLRSGDLDLNVRDADLNWIKACEVHQFG 60
PR	11-AUG-1999;	99US-0148319P.	99US-0148319P.
PR	12-AUG-1999;	99US-0148341P.	99US-0148341P.
PR	13-AUG-1999;	99US-0148565P.	99US-0148565P.
PR	14-AUG-1999;	99US-0148884P.	99US-0148884P.
PR	16-AUG-1999;	99US-0149268P.	99US-0149268P.
PR	17-AUG-1999;	99US-0149175P.	99US-0149175P.
PR	18-AUG-1999;	99US-0149426P.	99US-0149426P.
PR	20-AUG-1999;	99US-0149722P.	99US-0149722P.
PR	20-AUG-1999;	99US-0149899;	99US-0149899;
PR	20-AUG-1999;	99US-0149723P.	99US-0149723P.
PR	23-AUG-1999;	99US-0149429P.	99US-0149429P.
PR	23-AUG-1999;	99US-0149302P.	99US-0149302P.
PR	25-AUG-1999;	99US-0150566P.	99US-0150566P.
PR	26-AUG-1999;	99US-0150884P.	99US-0150884P.
PR	27-AUG-1999;	99US-0151065P.	99US-0151065P.
PR	27-AUG-1999;	99US-0151066P.	99US-0151066P.
PR	30-AUG-1999;	99US-0151080P.	99US-0151080P.
PR	31-AUG-1999;	99US-0151103P.	99US-0151103P.
PR	01-SEP-1999;	99US-0151438P.	99US-0151438P.
PR	07-SEP-1999;	99US-0151530P.	99US-0151530P.
PR	10-SEP-1999;	99US-0152363P.	99US-0152363P.
PR	13-SEP-1999;	99US-0153073P.	99US-0153073P.
PR	15-SEP-1999;	99US-0153758P.	99US-0153758P.
PR	16-SEP-1999;	99US-0154018P.	99US-0154018P.
PR	20-SEP-1999;	99US-0154719P.	99US-0154719P.
PR	22-SEP-1999;	99US-0155139P.	99US-0155139P.
PR	23-SEP-1999;	99US-0155486P.	99US-0155486P.
PR	24-SEP-1999;	99US-0155651P.	99US-0155651P.
PR	28-SEP-1999;	99US-0156438P.	99US-0156438P.
PR	29-SEP-1999;	99US-0156396P.	99US-0156396P.
PR	04-OCT-1999;	99US-0157117P.	99US-0157117P.
PR	06-OCT-1999;	99US-0157753P.	99US-0157753P.
PR	07-OCT-1999;	99US-0157865P.	99US-0157865P.
PR	08-OCT-1999;	99US-0158039P.	99US-0158039P.
PR	12-OCT-1999;	99US-0158369P.	99US-0158369P.
PR	13-OCT-1999;	99US-0159233P.	99US-0159233P.
PR	13-OCT-1999;	99US-0159294P.	99US-0159294P.
PR	14-OCT-1999;	99US-0159285P.	99US-0159285P.
PR	14-OCT-1999;	99US-0159323P.	99US-0159323P.
PR	14-OCT-1999;	99US-0159331P.	99US-0159331P.
PR	14-OCT-1999;	99US-0159631P.	99US-0159631P.
PR	14-OCT-1999;	99US-0159632P.	99US-0159632P.
PR	18-OCT-1999;	99US-0159294P.	99US-0159294P.
PR	21-OCT-1999;	99US-0159584P.	99US-0159584P.
PR	21-OCT-1999;	99US-0160380P.	99US-0160380P.
PR	22-OCT-1999;	99US-0160767P.	99US-0160767P.
PR	22-OCT-1999;	99US-0160770P.	99US-0160770P.
PR	25-OCT-1999;	99US-0160980P.	99US-0160980P.
PR	25-OCT-1999;	99US-0161404P.	99US-0161404P.
PR	25-OCT-1999;	99US-0161405P.	99US-0161405P.
PR	26-OCT-1999;	99US-0161406P.	99US-0161406P.
PR	26-OCT-1999;	99US-0161350P.	99US-0161350P.
PR	26-OCT-1999;	99US-0161360P.	99US-0161360P.
PR	28-OCT-1999;	99US-0161361P.	99US-0161361P.
PR	28-OCT-1999;	99US-0161920P.	99US-0161920P.
PR	28-OCT-1999;	99US-0161922P.	99US-0161922P.
PR	29-OCT-1999;	99US-0162142P.	99US-0162142P.
Db	RESULT 8		
Db	ID ABR61588	standard; protein; 358 AA.	
Db	ID ABR61588	standard; protein; 358 AA.	
Db	XX	Z. mays cyclin D polypeptide.	
Db	AC ABR61588;		
Db	XX	15-JAN-2004 (first entry)	
Db	XX	DT 23-OCT-2003.	
Db	XX	DE Silk exsertion; plant; transformation; transgenic; cyclin D.	
Db	XX	KW cyclin D.	
Db	OS Zea mays.		
Db	XX	WO2003087313-A2.	
Db	PN	WO2003087313-A2.	
Db	XX	PD 08-APR-2003; 2003WO-US010544.	
Db	XX	PF 08-APR-2003; 2003WO-US010544.	
Db	XX	PR 08-APR-2002; 2002US-0370796P.	
Db	XX	PA (PION-) PIONEER HI-BRED INT INC.	
Db	PI Zinselmeier C, Helentjaris TG;		
Db	XX	WPI; 2003-845315/78.	
Db	DR N-PSDB; ACP58156.		
Db	XX	The invention relates to enhancing silk exertion in a Zea mays plant under stress, relative to a non-transformed Zea mays plant under stress, relative to a non-transformed Zea mays plant under stress, relative to its ancestor with a construct comprising a silk-specific or silk-preferred promoter operably linked to a polynucleotide encoding a polypeptide that increases cell division. The present sequence represents a Z. mays cyclin D, a polypeptide involved in cell division.	
Db	PS Sequence 358 AA;		
Db	XX	Query Match Best Local Similarity Score 39.6%; DB 7; Length 358;	
Db	Matches 143; Conservative 40.2%; Pred. No. 2.2e-01; Mismatches 59; Indels 81; Gaps 10;		
Db	Qy 10 LLCTESN-----VDEDEM-----IVDETEPLEIS-PQMG 37		
Db	12 LLCAEDNAAILGLDDGESESSWAATGAVADGILTEFP-----3		
Db	12 LLCAEDNAAILGLDDGESESSWAATGAVADGILTEFP-----3		
Qy	36 MGFSQSESEIIMVKEKQHLPSSDDYIKRLRSGDLDLNVRDADLNWIKACEVHQFG 95		

of the polynucleotide sufficient to modulate (increase or decrease) the CycD protein in the cell. The CycD protein is present in an amount sufficient to alter cell division, increase the number of cells dividing, improve transformation frequencies, alter cell growth, increase the growth rate, increase crop yield, alter plant height or size, enhance or inhibit organ (seed, root, shoot, ear, tassel, pollen, stamen) growth, produce organ ablation, produce partenocarpic fruits, produce male sterile plants, enhance embryogenic response, increase callus induction, provide positive selection, increase plant regeneration, alter the time that cells are arrested in G1 or G0 phase or in a particular cell cycle, improve response to environmental stress including dehydration, heat or cold, increase the number of pods per plant, increase the number of seeds per pod or ear, alter the lag time in seed development, provide hormone-independent cell growth, or increase the growth rate of cells in bioreactors. The level of CycD protein in the cells is transiently modulated by introducing CycD RNA or CycD polypeptides. All claimed polypeptides. All claimed

XX Sequence 358 AA;

Query Match 39.3%; Score 621.5; DB 3; Length 358;

Best Local Similarity 39.3%; Pred. No. 1e-59;

Matches 142; Conservative 59; Mismatches 74; Indels 81; Gaps 10;

Qy 10 LLCTESN----VDBDM-----IYDETPEIIS.PQMIG 37

Db 12 LIGAEENAAAILGELDDGEESSWAAAATPPRDTVAAAATGVAANDGLTERFLP-----63

Qy 38 FSQLSESEIITMEMVEKEKOHLPSPDDYIKRL--RSGIDLILNGRRDAINWIKACEVHQFG 95

Db 64 ---LSDDCCVATLVEKEVERHMPAEGILQKDQRRHGDLLAVRKDIDWIKVIEYNFA 119

Qy 96 PUCFCIAMYDPEISWHDLSKGKGMWQLQAVACSLAAKIEETVPMJDLQGDPQF 155

Db 120 PLTAVLSVNYLDRFLSTYEFPGRAMNTQJLAVACTSLASKEETVPLIPDLOVEAKF 179

Qy 156 VPEAKSYQRMELVLMNLKWLRLATTPCSYTRYFLKMSKCDQEPPTNLIRSLSQVIAST 215

Db 180 VPEGRTIKRMELVLSTLKWMMHAVTACSEVYFLKLSD-HGAPSLIARERSSDVLIST 238

Qy 216 TKGIDFLERPRSEAAAVAVALSVGELQRVHFDNSFSPLSILQKERVKIGEMIE----271

Db 239 AKGAEEFVVFRBELLASAVLAAGRCRSVTERAASSCKY--LDKERVLRCHEMICKIT 296

Qy 272 ----SDGSPLCS--QTPNQVLEYSAC-----CFSFKTHDSSS 303

Db 297 AGSIVLKSAQSSSSVPQSPIGVDAACLSQSDDATVGSPAVCY----HSSSTS 348

RBSULT 10
RAY79322

RESULT 9
AYY79321 standard; protein; 358 AA.

ID AYY79321
XX AC AYY79321;
XX DT 18-JUL-2000 (first entry)
XX DE Maize cyclin D.
XX Maize; Cyclin D; ZmCycD; CycD; cell division; cell cycle;
XX KW transgenic plant.
XX OS WO200017364-A2.
XX PN WO200017364-A2.
XX PD 30-MAR-2000.
XX PR 21-SEP-1999; 99WO-US021946.
XX PR 23-SEP-1998; 98US-0101551P.
XX PA (PION-) PIONEER HI-BRED INT INC.
PI Lowe KS, Gordon-Kamm WJ, Gregory CA, McElver JA;
PI Hoerster GJ;
XX WPI: 2000-283589/24.
DR N-PSDB; AAZ24581.
XX Novel polynucleotides encoding maize cyclin D isoforms 1, 2 and 3, related proteins and antisense RNA useful for control of cell cycle regulation.
XX Claim 16; Page 117-118; 13pp; English.
XX DR 2000-283589/24.
XX Maize; cyclin D; ZmCycD; CycD; cell division; cell cycle;
XX PT AYY79322;
XX PR 18-JUL-2000 (first entry)
XX DE Maize cyclin D.
XX Maize; cyclin D; ZmCycD; CycD; cell division; cell cycle;
XX KW transgenic plant.
XX OS WO200017364-A2.
XX PN 99WO-US021946.
XX PR 23-SEP-1998; 98US-0101551P.
XX (PION-) PIONEER HI-BRED INT INC.

The present sequence is that of an isoform of maize cyclin D (CycD), a protein necessary for progression from G1 into S phase. CycD binds to CDK4, and the active CycD-CDK4 hyperphosphorylates retinoblastoma associated protein, releasing the E2F transcription factor which activates DNA synthesis. The invention provides maize CycD polynucleotides (see AAZ24581-84) and polypeptides (see AYY79321-24) that are involved in cell cycle regulation. Also provided are recombinant expression cassettes (including ZmCycD in sense or antisense orientation), host cells, transgenic plants (especially corn, sorghum, sunflower, safflower, wheat, rice, alfalfa or oilseed Brassica) and antibody compositions. A claimed method of modulating the level of CycD protein in a cell comprises transforming the cell with a recombinant expression cassette comprising a CycD polynucleotide linked to a promoter, and growing the cell for a time sufficient to induce expression

XX	Lowe KS, Tao Y, Gordon-Kamm WJ, Gregory CA, McElver JA;	Db	297 MGSTIVLKSAGSSISSVQSPSPIGVLDAAACLSQQDDATVGSPAVCY---HSSSTS 348
PI	WPI; 2000-283589/24.	RESULT 11	
PI	DR N-PSDE; AA594582.	AY79323	
XX	Novel polynucleotides encoding maize cyclin D isoforms 1, 2 and 3, related proteins and antisense RNA useful for control of cell cycle regulation.	ID AAY79323 standard; protein; 390 AA.	
PT	PT PT	XX	
XX	Claim 16; Page 121-122; 134pp; English.	AC AAY79323;	
PS		XX	
XX	The present sequence is that of an isoform of maize cyclin D (Cyclin D) (CycD), a protein necessary for progression from G1 into S phase. CycD binds to CDK4, and the active Cyclin-CDK4 hyperphosphorylates retinoblastoma associated protein, releasing the E2F transcription factor which activates DNA synthesis. The invention provides maize CycD polynucleotides (see AA79321-64) and polypeptides (see AA79321-24) that are involved in cell cycle regulation. Also provided are recombinant expression cassettes (including ZmCycD in sense or antisense orientation), host cells, transgenic plants (especially corn, sorghum, sunflower, safflower, wheat, rice, alfalfa or oilseed Brassica) and antibody compositions. A claimed method of modulating the level of CycD protein in cell comprises transforming the cell with a recombinant expression cassette comprising a CycD polynucleotide linked to a promoter, and growing the cell for a time sufficient to induce expression of the polynucleotide sufficient to modulate (increase or decrease) the CycD protein in the cell. The CycD protein is present in an amount sufficient to alter cell division, increase the number of cells dividing, improve transformation frequencies, alter cell growth, increase the growth rate, increase crop yield, alter height or size, enhance or inhibit organ (seed, root, shoot, ear, tassel, stalk, pollen, stamen) growth, produce organ ablation, produce parthenocarpic fruits, produce male sterile plants, enhance embryogenic response, increase callus induction, provide positive selection, increase plant regeneration, alter the time that cells are arrested in G1 or G0 phase or in a particular cell cycle, improve response to environmental stress including dehydration, heat or cold, increase the number of pods per plant, increase the number of seeds per pod or ear, alter the lag time in seed development, provide hormone-independent cell growth, or increase the growth rate of cells in bioreactors. The level of CycD protein in the cells is transiently modulated by introducing CycD RNA or CycD polypeptides. All claimed	XX	
XX	Sequence 358 AA;	XX	
SQ	Query Match Score 620.5; DB 3; Length 358; Best Local Similarity 39.9%; Pred. No. 1.3e-59; Matches 142; Conservative 59; Mismatches 74; Indels 81; Gaps 10;	XX	
QY	10 LLCTESN----VDDGEM-	37	
Db	12 LLLCAAAIAGLDDDESESSAAAATPPRDTVAAAATGAVDGLITEFL-----	63	
QY	38 FQSOSSEBEIIMVEKEKQHPLPDDDVIKRL--RSGDLDLNLYGRDNLWIKACEVHQFG 95 64 ---LSDCIVATLVEEVENHAEGLQKLQRHRGDLIVAVRKDAIDWIKWVTHYNEA 119	CC	
Db	96 PLCFCLAMNYDIDFLSVHDLPKGKGNWLIQOLLAVALAASLAAKIEETEVPMILDQYGPQF 155 120 PLTAVLSWYDRLFLSTYFPPGRAMNTQLLAVACSLASKIEETVPLPDQVAEAKF 179	CC	
QY	156 VPEAKSTORMELIVLNKWKWRAITPCSYFRKMSKDQEESPNTLIRSLSQYIAST 215	CC	
Db	180 VPEGRTIKRMELIVLNKWKWHAATCFSVYFLKRLSD-HGAPSLLARSDDIVLST 238	CC	
QY	216 TKGIDFLERPFSEAAAVALAVALSGLORVHDNSSESPLFLSQQKERVKGEME---	CC	
Db	239 AKGAEEFYVRPSEIAAVALAAGECRSSVIERAASSCKY-LDKERVLRCHEMIOEKIT 296	CC	
QY	272 -----SDGSPLCS--QTPNQVLEVSAC-----CFSFKTDSSSS 303	XX	
SQ	Sequence 390 AA;	Sequence 390 AA;	

Query Match Similarity 35.0%; Best Local Similarity 39.1%; Matches 135; Conservative 52; Mismatches 89; Indels 69; Gaps 9;	Score 554.5; Pred. No. 3.1e-32; Score 554.5; Pred. No. 3.1e-32;	Length 390; Length 390;	CC altered levels of the cyclin protein in a transformed host cell. This would have the effect of altering the regulation of cell division in those cells. The nucleic acid fragments may be used to express cyclins in plant cells to enhance cell tissue culture growth. The availability of nucleic acid sequences encoding all or a portion of cyclins should facilitate studies of cell cycle in plants, provide genetic tools to enhance cell growth in tissue culture, increase the efficiency of gene transfer and help provide more stable transformations. The proteins can be used as targets to facilitate design and/or identification of herbicides inhibitors of those enzymes that may be useful as herbicides
Qy 10 LICTEESNVD----DEGMIVDDEPIELTSIPIQMGSQS-----ESBEITIMEMVEK 53	Db 13 LUCABEERISSILWYDE---EEBEELEAVGRERRSPGYYGDFFGADLPPQSEBCVAGLVER 68	XX	XX
Qy 54 EKQHLPSDDYIKRIRSGLDIDNGRDLANINWKAACEBVHQFSPLCFLCLAMANYLDREFLSVH 113	Db 69 ERDHMPGPYCIGDRLRGGCGCLUCY-VREDAVDWIKWAKTHRFPLTAYLVANYLDRDSLGS 127	XX	XX
Qy 114 DLPSGKWIQLLIAVACULSLAAKIEETEPMLLDLQVGDPQKVFEAKSVQRNELLVNLK 173	Db 128 EVPDGKDWMTQQLLAVACULSLAAKMEETAVPQCLDQVGDARYFEAKTVQRNELLVNLTL 187	Sequence 388 AA;	Sequence 388 AA;
Qy 174 KWRLRAITPCSYTRFLRKMSK-CDQEFSNTLISRLQVIASTTKGIDFLFELFRPSEAAA 232	Db 188 NWRMHAUTPFSVTDYFLINKLNSGSTARSCWLQSAELLLRAARGTGCVGRPSETAA 247	Query Match 33.6%; Best Local Similarity 42.3%; Matches 124; Conservative 50; Mismatches 74; Indels 45; Gaps 8;	Query Match 33.6%; Best Local Similarity 42.3%; Matches 124; Conservative 50; Mismatches 74; Indels 45; Gaps 8;
Qy 233 VALSVSGFLQR-----VHDNSSSFSPFLSLLQKERVKKIGEMTESGSDLC---- 278	Db 248 VAAVAGDVVDDADGVENACAHVD-----KERVLCQEAGTMASSAAATDGDA 295	Db	Db
Qy 279 -----SQTPTNGYLEVSACCFSPKTXTHDSSS 303	Db 296 TVPPKSARRRSSPVPPVPPQSPVGVLD-AAACLTSYRSEEAATA 339	Qy 42 ESEEIIMEMVEKEKQHLPSDDYIKRURSGDIDLNVGRDALINWIAACEBVHQFSPLCFL 101	Qy 42 ESEEIIMEMVEKEKQHLPSDDYIKRURSGDIDLNVGRDALINWIAACEBVHQFSPLCFL 101
Qy 220 DFLERFSEAAAVALSVGELQ-----VHFDNSSPSPFLFLQKERV---KKI 266	Db 236 GCVGFERPESEIAAAVAVALAVGDDAGVENCACAHVD-----KERVLCQEAI 283	Db	Db
Qy 267 GEMIESPGSDLCS-----QTPNGVILBEVSACCFSEFTHDSSSS 303	Db 284 GSMASSAIDDAVTVPKSARRRSSPVPPQSPVGVLD-AAFCLSYRSEEAATA 335	Qy 57 QSEBECVAGLVERERDAMPGCPYGDRLRGGGCLCV RREADWIKWAKTHRFPLTAYL 115	Qy 57 QSEBECVAGLVERERDAMPGCPYGDRLRGGGCLCV RREADWIKWAKTHRFPLTAYL 115
RESULT 12 AAY31897	RESULT 13 AAG29789	XX	XX
ID AAY31897 standard; protein; 388 AA.	ID AAG29789 standard; protein; 328 AA.	AC	AC
XX	XX	XX	XX
XX	XX	DT 17-OCT-2000 (first entry)	DT 17-OCT-2000 (first entry)
XX	XX	XX	XX
XX	XX	DE Arabidopsis thaliana Protein Fragment SEQ ID NO: 35502.	DE Arabidopsis thaliana Protein Fragment SEQ ID NO: 35502.
XX	XX	KW Protein transduction pathway; metabolic pathway;	KW Protein transduction pathway; metabolic pathway;
XX	XX	KW hybridisation assay; genetic mapping; gene expression control; promoter; terminatin sequence.	KW hybridisation assay; genetic mapping; gene expression control; promoter; terminatin sequence.
XX	XX	OS Arabidopsis thaliana.	OS Arabidopsis thaliana.
XX	XX	EN EP1033405-A2.	EN EP1033405-A2.
XX	XX	PD 06-SEP-2000.	PD 06-SEP-2000.
XX	XX	PF 25-FEB-2000; 20000EP-00301439.	PF 25-FEB-2000; 20000EP-00301439.
XX	XX	PR 25-FEB-1999; 99US-0121835P.	PR 25-FEB-1999; 99US-0121835P.
XX	XX	PR 05-MAR-1999; 99US-0123160P.	PR 05-MAR-1999; 99US-0123160P.
XX	XX	PR 09-MAR-1999; 99US-0123548P.	PR 09-MAR-1999; 99US-0123548P.
XX	XX	PR 23-MAR-1999; 99US-015788P.	PR 23-MAR-1999; 99US-015788P.
XX	XX	PR 23-MAR-1999; 99US-0126264P.	PR 23-MAR-1999; 99US-0126264P.
XX	XX	PR 29-MAR-1999; 99US-0126778P.	PR 29-MAR-1999; 99US-0126778P.
XX	XX	PR 01-APR-1999; 99US-0127462P.	PR 01-APR-1999; 99US-0127462P.
XX	XX	PR 06-APR-1999; 99US-0128234P.	PR 06-APR-1999; 99US-0128234P.
XX	XX	PR 16-APR-1999; 99US-0129845P.	PR 16-APR-1999; 99US-0129845P.
XX	XX	PR 21-APR-1999; 99US-0130077P.	PR 21-APR-1999; 99US-0130077P.
XX	XX	PR 23-APR-1999; 99US-0130510P.	PR 23-APR-1999; 99US-0130510P.
XX	XX	WPI; 1999-591036/50.	WPI; 1999-591036/50.
XX	XX	DR N-PSDB; AAZ19961.	DR N-PSDB; AAZ19961.
XX	XX	New isolated plant cyclin genes, used to develop products for use as herbicides and for developing plant breeding programs.	New isolated plant cyclin genes, used to develop products for use as herbicides and for developing plant breeding programs.
XX	XX	Claim 11; Page 56-57; 68pp; English.	Claim 11; Page 56-57; 68pp; English.
XX	XX	This is the deduced amino acid sequence of a corn cyclin delta-2 protein derived from the nucleotide sequence (see AAZ19961) of a clone from an embryo leaf cDNA library. It represents 94% of the full-length protein. The invention relates to isolated nucleic acid fragments (see AAZ19953-66) encoding cyclin A, cyclin delta-1, cyclin delta-2 and cyclin delta-3 polypeptides (see AAY31889-302). It also relates to the construction of chimeric genes encoding all or a portion of a cyclin, in sense or antisense orientation, where expression of the chimeric gene results in	This is the deduced amino acid sequence of a corn cyclin delta-2 protein derived from the nucleotide sequence (see AAZ19961) of a clone from an embryo leaf cDNA library. It represents 94% of the full-length protein. The invention relates to isolated nucleic acid fragments (see AAZ19953-66) encoding cyclin A, cyclin delta-1, cyclin delta-2 and cyclin delta-3 polypeptides (see AAY31889-302). It also relates to the construction of chimeric genes encoding all or a portion of a cyclin, in sense or antisense orientation, where expression of the chimeric gene results in

PR	23-APR-1999;	99US-0130891P.	99US-0144884P.
PR	28-APR-1999;	99US-0131449P.	99US-0144814P.
PR	30-APR-1999;	99US-0132040P.	99US-0145086P.
PR	04-MAY-1999;	99US-0132407P.	99US-0145088P.
PR	05-MAY-1999;	99US-0132484P.	99US-0145085P.
PR	06-MAY-1999;	99US-0132485P.	99US-0145087P.
PR	06-MAY-1999;	99US-0132486P.	99US-0145089P.
PR	07-JUN-1999;	99US-0132487P.	99US-0145192P.
PR	11-MAY-1999;	99US-0132463P.	99US-0145145P.
PR	14-MAY-1999;	99US-0134456P.	99US-0145199P.
PR	20-MAY-1999;	99US-0134218P.	99US-0145218P.
PR	21-MAY-1999;	99US-0134219P.	99US-0145224P.
PR	24-MAY-1999;	99US-0134221P.	99US-0145267P.
PR	14-MAY-1999;	99US-0134221P.	99US-0145913P.
PR	18-MAY-1999;	99US-0134730P.	99US-0145919P.
PR	19-MAY-1999;	99US-0134768P.	99US-0145919P.
PR	20-MAY-1999;	99US-0134911P.	99US-0146386P.
PR	01-JUN-1999;	99US-0135124P.	99US-0146388P.
PR	03-JUN-1999;	99US-0135333P.	99US-0146389P.
PR	04-JUN-1999;	99US-0135333P.	99US-0147038P.
PR	25-MAY-1999;	99US-0136021P.	99US-0147416P.
PR	27-JUN-1999;	99US-0136312P.	99US-0147204P.
PR	28-MAY-1999;	99US-0136782P.	99US-0147302P.
PR	01-JUN-1999;	99US-0137222P.	99US-0147192P.
PR	04-JUN-1999;	99US-0137528P.	99US-0147260P.
PR	07-JUN-1999;	99US-0137724P.	99US-0147303P.
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RESULT 15
AAG29790

ID AAG29790 standard; protein; 320 AA.
AC AAG29790;

DB 17-OCT-2000 (first entry)

Arabidopsis thaliana protein fragment SEQ ID NO: 35503.

XX Protein identification; signal transduction pathway; metabolic pathway;
 KW hybridisation assay; genetic mapping; gene expression control; promoter;
 KW termination sequence.

XX *Arabidopsis thaliana*.

OS EP1033405-A2.

XX PR 25-FEB-1999; 99US-0121825P.
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 PF PR 05-MAR-1999; 99US-0123180P.
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Db 279 SVRASSSTTRPDES 293

Search completed: March 23, 2004, 16:37:35
Job time : 64 secs

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Patent No. 6559358
 GENERAL INFORMATION:
 APPLICANT: MURRAY, James Augustus Henry
 TITLE OF INVENTION: PLANTS WITH MODIFIED GROWTH
 FILE REFERENCE: 212-1-015.P
 CURRENT APPLICATION NUMBER: US/09/404,296B
 CURRENT FILING DATE: 1999-09-24
 NUMBER OF SEQ ID NOS: 32
 SOFTWARE: PatentIn version 3.1
 LENGTH: 361
 TYPE: PRT
 ORGANISM: Arabidopsis thaliana
 US/09-404-296B-30

Query Match 40.1%; Score 635.5; DB 4; Length 361;
 Best Local Similarity 42.8%; Pred. No. 6.9e-65; Indels 73; Gaps 12;
 Matches 154; Conservative 58; Mismatches 75;

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 Db 53 PONGFSSSSSLSDERIKEWMLVREIEFCPTDYYKVRLLSGDLDLSV-RNOALDWLWKCAHY 111

RESULT 4
 US-09-398-858-12
 Sequence 12, Application US/093988858
 Patent No. 6518487
 GENERAL INFORMATION:
 APPLICANT: Low, Yumin
 APPLICANT: Gordon-Kamm, William J.
 APPLICANT: Gregory, Carolyn A.
 APPLICANT: McElver, John A.
 APPLICANT: Hoerster, George J.
 TITLE OF INVENTION: Cyclin D Polynucleotides, Polypeptides
 FILE REFERENCE: 0946
 CURRENT APPLICATION NUMBER: US/09/398,858
 PRIOR APPLICATION NUMBER: 60/101,551
 PRIOR FILING DATE: 1998-09-23
 NUMBER OF SEQ ID NOS: 30
 SOFTWARE: FastSEQ for Windows Version 3.0
 SEQ ID NO 12
 LENGTH: 358
 TYPE: PRT
 ORGANISM: Zea mays

US-09-398-858-12

Query Match 39.2%; Score 620.5; DB 4; Length 358;
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RESULT 4
 US-09-398-858-12
 Sequence 12, Application US/093988858
 Patent No. 6518487
 GENERAL INFORMATION:
 APPLICANT: Low, Yumin
 APPLICANT: Gordon-Kamm, William J.
 APPLICANT: Gregory, Carolyn A.
 APPLICANT: McElver, John A.
 APPLICANT: Hoerster, George J.
 TITLE OF INVENTION: Cyclin D Polynucleotides, and Methods of Use
 FILE REFERENCE: 0946
 CURRENT APPLICATION NUMBER: 1999-09-20
 PRIOR APPLICATION NUMBER: 60/101,551
 PRIOR FILING DATE: 1998-09-23
 NUMBER OF SEQ ID NOS: 30
 SOFTWARE: FastSEQ for Windows Version 3.0
 SEQ ID NO 12
 LENGTH: 358
 TYPE: PRT
 ORGANISM: Zea mays

US-09-398-858-12

Query Match 39.2%; Score 620.5; DB 4; Length 358;
 Best Local Similarity 39.9%; Pred. No. 3.7e-63; Mismatches 74; Indels 81; Gaps 10;

Qy 10 LLCTEN-----VDEGM-----
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 Qy 38 PSQSESEETIMEMVEKERHOLPSDDYIKRL--RGSQLDLNVGRDAUNWIKACEVHOFG 95
 Db 64 ---ISDDCVATLVEKEVHMPARGYLQRHGDLLAVRKDAIDWIKVIEHNFA 119
 Qy 96 PLCFCLAMNYLDRFLPSGKWMVLLQQLAYACSLAAKIEETVPMILIDQVGDQF 155
 Db 120 PLTAVLSVNLDRFLSTYEFPGRAMNTQQLAYACSLASKIEETVPLPDLQVAAKF 179
 Qy 156 VFEAKSTORMELVLLNKLMKRLRATTPCSYTRYFLRMSKCDQEPNTLISRSLQVIAST 215
 Db 180 VFEGRATIKRMELVLLTKWRAHATCFSFVEYLFLKLSD-HGAPSLARSSSDVLST 238
 Qy 216 TKGIDFLERPSBAAAVALSVSGETQVHDNSSPSFSLQKERVKKIGEMIE---271

RESULT 5

US-09-398-858-14

Query Match Score 28.0%; Score 443.5%; DB 4; Length 335;

Best Local Similarity 37.0%; Pred. No. 1..1e-42;

Matches 117; Conservative 53; Mismatches 105; Indels 41; Gaps 11;

; SEQ ID NO: 28

; LENGTH: 335

; TYPE: PRT

; SOFTWARE: PatentIn version 3.1

Qy 7 ELSLICTEVNDDGMIIVDETPIBISIPOMGFSOSESE---EETIMEMVEKEKOHLPSPDD 62

Db 19 DMDIFCQE---DSGVFSEGSTVD----FSSEVDSWPGDIACTFEDERFVFGD 67

Qy 63 YIKRURSGDLDLNWGRDAINWIKACEYHQFGPLCFCLAMNYLDRFLSYHDLPSKGKWTI 122

Db 68 YLSRFQTRSDas-AREDSEVAWILKQVQATYNFQPLTAYIAVNMDFRLYARRLBTSGPB 126

Qy 123 LOLIANACSLAAKIEETEYPMILDQVDFPEAKSVMQMLVNLKLRALATP 182

Db 127 MOLLAVACSLAAKMEELLVPSLDFEVAGVKYLFEAKTIGRMELVLVSVDWLRLSVP 186

Qy 183 CSYTRFLRKMSKCDQEPESTN---LISRSLLQVIASTTKGIDFLEFRPPEAAAVALSVS 238

Db 187 FDESFPEAKI---DPSCTELGFFSHATEIILSYKEASLEYWPSIAANALCYA 241

Qy 239 GELORVHFNDNSFSPLFSL---LOKERVKKGIGEMIES---DGSDLCSQTPNGV--LE 287

Db 242 NELPSL---SSVNVPHESPETWDGLSKESKEVCRYLKMATAENRNL-NTPKVIAKUR 296

Qy 288 VSACCFSEKTHDSSS 303

Db 297 VSVRASSTLTPSPDES 312

Qy RESULT 7

US-09-404-296B-8

; Sequence 8, Application US/09404296B

; Patent No. 6559358

; GENERAL INFORMATION:

; APPLICANT: MURRAY, James Augustus Henry

; TITLE OF INVENTION: PLANTS WITH MODIFIED GROWTH

; FILE REFERENCE: 2121-0151P

; CURRENT APPLICATION NUMBER: US/09/404,296B

; CURRENT FILING DATE: 1999-09-24

; NUMBER OF SEQ ID NOS: 32

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO: 8

; LENGTH: 315

; TYPE: PRT

; ORGANISM: Hejlianthus tuberosus

US-09-404-296B-8

Query Match Score 27.8%; Score 440.5%; DB 4; Length 315;

Best Local Similarity 36.6%; Pred. No. 2..3e-42;

Matches 111; Conservative 59; Mismatches 102; Indels 31; Gaps 9;

Qy 10 LLCTESNVD---DEGMIVDETPIBISIPOMGFSOS-----ESEETIMEMYEK 53

Db 13 LLCADEHSS-TLWDE---DEEEELAVERGRGRGRSPGYDDGADLFPQOECVAGLVER 68

Qy 54 EKOHLPSDDYIKRLRGSGDLDLNWGRDAINWIKACEYHQFGPLCFCLAMNYLDRFLSYH 113

Db 69 ERDMPGPGCYDRGGGGCICV-RREAVWIKAYTHEFRPTAYLAVNLYLDRFLSIS 127

Qy 114 DLPSKGWIIOLLAVALAACAKIEETEYPMILDQVDFPEAKSVMQMLVNL 173

Db 128 EVPDGKDWWMQLLAVALCACSLAAKMEETAVPQCLDQVGDRARYPEAKTVQRMELVLTY 187

Qy 174 KWRRAITPCSYTRFLRKMSK-CDQEPESTNLLRSLOYIASTTKGIDFLEFRPSEAAA 232

Db 188 NWRMHEAVTPSYVDYFLNKLSNGGSTAPRSCWLLOSAELLAARGTGCGRPSEIAAA 247

Qy 233 VALSYSGEQR-----VHFNDNSSFSPLFSLJQKERVKKIGEMIESGSDLIC---- 278

Db 248 VAAAVAGDVADGYNACAHVD-----KERTLCOBAGNSAAGDA 295

Qy 279 -----SOTPNQVLEYSACCPSFKTHDSSS 303

Db 296 TVPPKSARRRSSPVVPPVPPQSPVGVLD-AAACLSYRSEATA 339

RESULT 6

US-09-404-296B-28

; Sequence 28, Application US/09404296B

; Patent No. 6559358

; GENERAL INFORMATION:

; APPLICANT: MURRAY, James Augustus Henry

; TITLE OF INVENTION: PLANTS WITH MODIFIED GROWTH

; CURRENT APPLICATION NUMBER: US/09/404,296B

; CURRENT FILING DATE: 1999-09-24

Qy 69 SGDLDLNWGRDAINWIKACEYHQFGPLCFCLAMNYLDRFLSPGKWMILQJLAV 128

Db 65 SQVLDas-AEESVAVILKQVQTFYCRGFVYANGWPLQLSV 123

Qy 129 ACLSLAAKIEETEYPMILDQVDFPEAKSVMQMLVNLKLRALATPCSYTRI 188

Db 124 ACLSLAAKMEETLIPSLDQVEGAKY.FEPTKIRMFELVLSVLDLRLSUTPFSGF 183

Qy 189 FLRKMSKCDQEPESTN---LISRSLLQVIASTTKGIDFLEFRPSEAAAVALSVSGEJORV 244

RESULT 8
US-09-404-296B-32
; Sequence 32, Application US/09404296B
; Patent No. 6559358
; GENERAL INFORMATION:
; APPLICANT: MURRAY, James Augustus Henry
; TITLE OF INVENTION: PLANTS WITH MODIFIED GROWTH
; FILE REFERENCE: 2121-0151P
; CURRENT APPLICATION NUMBER: US/09/404,296B
; CURRENT FILING DATE: 1999-09-24
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 32
; LENGTH: 376
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-09-404-296B-32

Query Match 23.9%; Score 379; DB 4; Length 373;
Best Local Similarity 31.0%; Pred. No. 4e-35%;
Matches 113; Conservative 94; Indels 92; Gaps 17;

Qy 4 ENLELS-----LCTESN-----VDDGGMIVDEDEPI--EIS-----IPQM 36
Db 7 EQQEELQSFLIDALYCEEEEEEKGWDIVDDETTI---TPLSSEVTTTTTKPNSLPLLI 63

Qy 37 GFSQS--ESEBIIIMVEKEQHLSDDYKRLRSGLDNLNVGRDNLWNIWKAECVHQ 93
Db 64 LLEQDLFWDEDELLSFSKEKETHOWNSF----QDDSLUCLSRDVSWEILKVNQGYG 118

Qy 94 FGPLCFCCLANNYLDREPLSVIDLPSGGKWIIQLLAVALAACLTEEVPMILIDLVQGDGP 153
Db 119 FSALTAVLAMYFDREPLTSHYQDXPKWMQLAAVTCLSAAKVEETQVPLLLDFQVEDA 178

Qy 154 QFVFEAKSVORMELLYLNKLKWRLRATAPCSYIRYFLRKMS-----KCQDEPSN 202
Db 179 KVVFEXTIQRNEMLLTSSLRKRNNTVTPSLFDHTRRLGRNNIHWEPRLRCE----N 234

Qy 203 TLISRSLQVIASSTKGDILEFRPSEAAAVALSYSGELQ--RVHDNDSSFSPLFSLLQ
Db 235 LILS----INADCR---FVRMPSVTLATAMLYHVQEPNCNSTDYQONQLLGVIL-KIN 284

Qy 260 KERVKIGEMIESDGGDLCSO-----TPNGVLEVSACCCSFKTH----DS 300
Db 285 KEKVNNCFELI---SEVCSPKRSPISHKRYKENPSHSPSGVIDP--IYSSESSNDSWDLLES 337

Qy 301 SSSY 304
Db 338 TSSY 341

RESULT 10
US-09-404-296B-6
; Sequence 6, Application US/09404296B
; Patent No. 6559358
; GENERAL INFORMATION:
; APPLICANT: MURRAY, James Augustus Henry
; TITLE OF INVENTION: PLANTS WITH MODIFIED GROWTH
; FILE REFERENCE: 2121-0151P
; CURRENT APPLICATION NUMBER: US/09/404,296B
; CURRENT FILING DATE: 1999-09-24
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 6
; LENGTH: 367
; TYPE: PRT
; ORGANISM: Nicotiana tabacum
US-09-404-296B-6

Query Match 23.4%; Score 370; DB 4; Length 367;
Best Local Similarity 32.3%; Pred. No. 3.8e-34%;
Matches 97; Conservative 62; Indels 84; Gaps 10;

Qy 42 ESEBIIIMVEKEQHLSDDYKRLRSGLDNLNVGRDNLWNIWKAECVHQGPLCFCL 101
Db 58 EDDQVLVLLTKEKESHLGFCOLIS--DGDGFLYEVRKEARLDWMLRVIAHYGEFAMTAVL 114

Qy 102 AMNYLDRFLSVHDLPSKGWNLQLLAVACLSAAKTEEVPMILDQVGDPMQFVFEAKS 161
Db 115 AVNYFFRFVSGLCQDKPMWSQLAVALAACLTEEVPMILDQVGDPMQFVFEAKT 174

Qy 162 VORMELLYLNKLKWRLRATAPCSYIRYFLRK-----MSKCDQEPSNTLIRSRLQ 210
Db 175 IQRMBELVLSLKWNPNVPLSFDHIMERGFPTNLHDFLRCR----LI---LG 226

Qy 211 VIASTTGKGDILEFRPSEAAAVALSYSGELQ--RVHDNDSSFSPLFSLLQKERVKK-- 265
Db 227 IITDSR---LHHYPPSVIATAVYYFVINIEPCNAMEXQNQMTVL-----KVKQDS 275

RESULT 9
US-09-404-296B-4
; Sequence 4, Application US/09404296B
; Patent No. 6559358
; GENERAL INFORMATION:
; APPLICANT: MURRAY, James Augustus Henry
; TITLE OF INVENTION: PLANTS WITH MODIFIED GROWTH
; FILE REFERENCE: 2121-0151P
; CURRENT APPLICATION NUMBER: US/09/404,296B
; CURRENT FILING DATE: 1999-09-24
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 4
; LENGTH: 373
; TYPE: PRT

RESULT 11
 US 09-404-296B-10
 Sequence 10, Application US/09404296B
 Patent No. 6559358
 GENERAL INFORMATION:
 APPLICANT: MURRAY, James Augustus Henry
 TITLE OF INVENTION: PLANTS WITH MODIFIED GROWTH
 CURRENT APPLICATION NUMBER: US/09/404,296B
 CURRENT FILING DATE: 1999-09-24
 NUMBER OF SEQ ID NOS: 32
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO 10
 LENGTH: 357
 TYPE: PRT
 ORGANISM: Helianthus tuberosus
 US-09-404-296B-10

Query Match Score 22.6%; Score 357.5; DB 4; Length 357;
 Best Local Similarity 31.1%; Pred. No. 1.2e-32; Mismatches 65; Indels 114; Gaps 12;
 Matches 101; Conservative 65; Matches 114; Indels 45; Gaps 12;

QY 9 SLLCTES-----NVDDB-----GMIVDTEPIE-SIPOMGFSQSESERIMVKEKQ 56
 Db 14 TLFNEQQDHEYHEYEBOFTQTLTDSDLHPPDLDLSWEHEELVSLTKBQSQ 73

QY 57 -HLPSSDDY-KRILRGSDLDUNV-GRRDALNWKFACEHQGFLCFLAMNYLDRFSLW 113
 Db 74 KOTPC-----TLSGKTSSVFAARKEADTWLKVSCYGETPTAILNWKDRFSSL 128

QY 114 DLPSGKGWMQLQVAVCLSLAAKETEENPMLIDQVGDFQYFEAKSVORMELLVNLK 173
 Db 129 HFQDKPWNMQLQVAVCLSLAAKETEENPMLIDQVGDFQYFEAKSVORMELLVNLK 188

QY 174 KWRLRAITPGSYTFLRMSKCDQEPNTLISRSLOVIASTTKGIDFBLQVETKYLFEAKNVORMELLVNLK 233
 Db 189 KWRNAPNPTVPSLFDHVRLGTLDHWD-FPKKCEAM-LCLYSDSRFTCYKSVLATP 247

QY 234 AIVSGEGLQRVHEDNSSFSPLESIQL-Q-KERVKIGEMI-----ESDGSDLCSQ 280
 Db 248 MLHYVDEIDPNCDYK-SQDLIKTTDINECYELTVELAYDHNNRKHDANETTN 306

QY 281 -TPNGVLEVSACCSEFHKTDSSS 303
 Db 307 PVSPAGVIDE-----TCDESSN 323

RESULT 12
 US 09-398-858-22
 Sequence 22, Application US/09398858
 Patent No. 6518487
 GENERAL INFORMATION:
 APPLICANT: Low, Keith S.
 APPLICANT: Tao, Yunlin
 APPLICANT: Gordon-Kamm, William J.
 APPLICANT: Gregory, Carolyn A.
 APPLICANT: McElver, John A.
 APPLICANT: Hoerster, George J.
 TITLE OF INVENTION: Cyclin D Polynucleotides, Polypeptides
 FILE REFERENCE: 0926
 CURRENT APPLICATION NUMBER: US/09/398,858
 CURRENT FILING DATE: 1999-09-20
 PRIOR APPLICATION NUMBER: 60/101,551
 PRIOR FILING DATE: 1998-09-23
 NUMBER OF SEQ ID NOS: 30
 SOFTWARE: FastSEQ for Windows Version 3.0

Query Match Score 18.4%; Score 291.5; DB 4; Length 349;
 Best Local Similarity 31.1%; Pred. No. 5.1e-25; Mismatches 96; Indels 27; Gaps 5;
 Matches 101; Conservative 31.1%; Pred. No. 5.1e-25; Mismatches 96; Indels 27; Gaps 5;

QY 10 LCTESTSNV-----DEGMIVDTEPIE-SIPOMGFSQSESERIMVKEKQH-----L 58
 Db 18 LICEDGSDLLADOGA-----GRDLVYARDERELVWQDEETVALLSKESASGGGPVE 74

QY 59 PSDDY-KRILRGSDLDUNV-GRRDALNWKFACEHQGFLCFLAMNYLDRFSLW 118
 Db 75 EMDWMMXARSQ-----CVRWLKTTAMFRFGKTAVAVNYLDRFLAQRVNRE 124

QY 119 KGWLQQLLAVACLSLAAKETEENPMLIDQVGDFQYFEAKSVORMELLVNLK 178
 Db 125 HAWGQLQIMVACMSLAAKETEENPMLIDQVGDFQYFEAKSVORMELLVNLK 184

QY 179 ATPPCSYTFLRMSKCDQEPNTLISRSLOVIASTTKGIDFBLQVETKYLFEAKNVORMELLVNLK 238
 Db 185 AVPPFYISCAAFER----QDERRAVLRAVECFVAAIRAMSSEYQFSTIAYASILYAR 241

RESULT 13
 US-08-770-761A-2
 Sequence 2, Application US/08770761A
 Patent No. 5814503
 GENERAL INFORMATION:
 APPLICANT: Kovacevic, Steven
 APPLICANT: Otto, Keith A.
 APPLICANT: Rao, Ramachandra N.
 APPLICANT: Title of Invention: FUSION PROTEINS COMPRISING CELL CYCLE
 NUMBER OF SEQUENCES: 8
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Eli Lilly and Company
 STREET: Lilly Corporate Center/Patent Division
 CITY: Indianapolis
 STATE: IN
 COUNTRY: USA
 ZIP: 46285
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/770,761A
 FILING DATE: 19-DEC-1996
 CLASSIFICATION: 530
 ATTORNEY/AGENT INFORMATION:
 NAME: Gaylo, Paul J.
 REGISTRATION NUMBER: 36,808
 REFERENCE/DOCKET NUMBER: X-10136
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 317-376-0756
 TELEFAX: 317-277-1917
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 660 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-08-770-761A-2

STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: Peptide
 US-08-464-517-20

Query Match 15.1%; Score 239.5; DB 2; Length 660;
 Best Local Similarity 28.5%; Pred. No. 1.5e-18;
 Matches 88; Conservative 51; Mismatches 115; Indels 55; Gaps 14;

Qy 1 MAEEN-----LEI.SILCTCBENVYDDEGMIVDETPIEISI.PQMGFQSEEEELINE 49
 Db 15 MAEOKLISEEDDLILAMEHQHLLCCRV--ET--IRRVDANIL--NDRVLA 60

Qy 50 MVEKEKOHLPSSDDYIKRLRGSDLDLNVRGRRDALNTWKAGEVHQFGLPCLMANNYLDRF 109
 Db 61 MLIKAETCAPIVSYSYFCVKEVPLPSM--RKIVATWNLVECEBQKCBEEVPLAMNYLDRF 118

Qy 110 LSVHDPLPSKGWLQLLAVACSLAIAKIEETEVPMILIDLVQGDPPQFVPEAKSVQ---R 164
 Db 119 ISLEPYTKSR --LQLIGATCMFVAISKMKET-IPL---TAEKLCIYTNSIRPEBLIQ 169

Qy 165 MELLVNKLKWLRLATTPCSTYFLRKMSKCDQEFSNTLISRSLOV-TASTTRKGIDFLE 223
 Db 170 MELLVNKLKWLRLAATMPDFLEHFLSKMP-EABENKQ1TRKAOTFVALCATDUKFIS 227

Qy 224 ERPS-EAAAYAVALSVGELQRYHFDNSFSPLSILQKERYKKIGEMIESDGSDL--CSQ 280
 Db 228 NPPSMYAGSVVAAVQNLNR-----SPNPNFLSYYRLTRFLSRVICKCDPDLRACQE 279

Qy 281 TPNGVLEVS 289
 Db 280 QIBALLESS 288

Query Match 15.0%; Score 237; DB 2; Length 295;
 Best Local Similarity 28.4%; Pred. No. 8.1e-19;
 Matches 83; Conservative 52; Mismatches 115; Indels 42; Gaps 13;

Qy 6 LEISLCLCTSNVDDDEGMIVDETPIEISI.PQMGFQSSESBEIIMVEKEKOHLPSSDDYIK 65
 Db 1 MENQLCCEV-----ET--IRRVDNTLL--NDRVLA 60

Qy 66 RLRSQDLDLNVRGRRDALNTWKAGEVHQFGLPCLMANNYLDRFSLVHDLPSCKGWLQIOL 125
 Db 47 CVOKEBIVPSM--RKIVATWNLVECEBQKCBEEVPLAMNYLDRFSLPELKKSRL--IQL 101

Qy 126 LAVACSLANKIETEVPLMLDVQGDPEVFEEKSVQ---RMELLVNKLKWLRLAI 180
 Db 102 LGATCMFVAISKMKET-IPL---TAEKLCIYTNSIRPEBLQMELLVNKLKWLNLAM 155

Qy 181 TPCSTYFLRKMSKCDQEFSNTLISRSLOV-TASTTRKGIDFLEFRPSAAAVALNSVG 239
 Db 156 TPHDTTEHFSKMP--DAEENKQ1TRKAOTFVALCATDUKFISMPPEMVAG--SMVA 210

Qy 240 ELQRTHFDNSFSPLSILQKERYKKIGEMIESDGSDL--CSQTNGVLEVS 289
 Db 211 AMQGNLGG---SPNPNFLSYRTTHFLSRVICKCDPDLRACQEQLAELESS 258

RESULT 15
 US-08-246-361A-20
 ; Sequence 20, Application US/08246361A
 ; Patent No. 59895B2
 ; GENERAL INFORMATION:
 ; APPLICANT: BEACH, David H.
 ; TITLE OF INVENTION: D-TYPE CYCLIN AND USES RELATED THERETO
 ; NUMBER OF SEQUENCES: 50
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: LAHIVE & COCKFIELD
 ; STREET: 60 State Street
 ; CITY: Boston
 ; STATE: MA
 ; COUNTRY: USA
 ; ZIP: 02109
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: ASCII (text)
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/246,361A
 FILING DATE: 19-MAY-1994
 CLASSIFICATION: 435
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 07/963,308
 FILING DATE: 16-OCT-1992
 APPLICATION NUMBER: US 07/888,178
 FILING DATE: 26-MAY-1992
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 07/464,517
 FILING DATE: 16-MAY-1991
 ATTORNEY/AGENT INFORMATION:
 NAME: Matthew P. Vincent
 REGISTRATION NUMBER: 36,709
 REFERENCE/DOCKET NUMBER: MII-004C
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (617) 227-7400
 TELEX/FAX: (617) 227-5941
 INFORMATION FOR SEQ ID NO: 20:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 295 amino acids
 TYPE: amino acids
 SEQUENCE CHARACTERISTICS:
 LENGTH: 295 amino acids
 TYPE: amino acids

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; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-246-361A-20

Query Match      15.0%; Score 237; DB 2; Length 295;
Best Local Similarity 28.4%; Pred. No. 8.1e-19;
Matches 83; Mismatches 115; Indels 42; Gaps 13;

Qy   6 LEISLCTESNVDDGGMIVDETPIEISIPIOMGSOSESEELIMEMVEKEKQHLPSDDYIK 65
Db    1 MENQLICCEV-----ET-TRAYPDTNL---NVRVLRLMLKTETCAPSVSYK 46

Qy   66 RLRSGDLDLNWGRDNLNWTKACEVHOFGLCFCIAMNYLDRFLSVDJPSGRGWILDQ 125
Db    47 CVQKETVPSM -RKTVATWMLLEVCEEQKCBEEVPLAMNTYLDREFLSLEPKKSR--LQL 101

Qy   126 LAVACISSLAAKIEETEVPMIJDLOQVDPQVFEAKSVQ-----RMELLVYLNKLERWLRRAI 180
Db    102 LGATCMFVAISKMKET-IP-L-----TAEKLCIYTDSIRPBEILLWNKLNILAM 155

Qy   181 TPCSYIRYFLRKMSKCDQEPSNTLISRSLQV-IASTTKGIDFLEFRPSEAAYAVALS VSG 239
Db   156 TPHDFLEHFLSKMP -DAEENKQIIRKAOTFVALCATDKFISNPSPSYAAG --SMVTA 210

Qy   240 ELQRVHFIDNSSTSPLSLLQGRVRKIGGMMESDSDL--ESQTENGVLVTS 289
Db   211 AMQGINLG---SPXNFLSRYRTTHFLSRVIKCDPDLRACQEQTAEALLSS 258

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Search completed: March 23, 2004, 16:40:15
 Job time : 24 secs

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OM protein - protein search, using sw model

Run on: March 23, 2004, 16:39:06 ; Search time 50 Seconds

1 MAEENIELSLCITESNVDDE.....SACCFSFKTHDSSSYTHLS 308
1595.165 Million cell updates/sec

Title: US-09-530-209A-2

Perfect score: 1583

Sequence: 1 MAEENIELSLCITESNVDDE.....SACCFSFKTHDSSSYTHLS 308

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1049977 seqs, 255955339 residues

Total number of hits satisfying chosen parameters: 1049977

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Published Applications_AA.*

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18: /cgcn2_6/_ptodata/1/_pubpaa/_US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the total score distribution, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	722.5	45.6	354	15	US-10-388-269-2
2	627.5	39.6	358	15	US-10-409-701-5
3	621.5	39.3	358	14	US-10-320-230-12
4	620.5	39.2	358	14	US-10-320-230-12
5	613.5	38.8	323	12	US-10-425-114-38749
6	595	37.6	345	12	US-10-425-114-53407
7	595	37.6	345	12	US-10-425-114-56939
8	585.5	37.0	340	12	US-10-425-114-49308
9	563.5	35.6	344	15	US-10-310-154-411
10	554.5	35.0	390	14	US-10-320-230-12
11	521.5	32.9	356	15	US-10-310-154-430
12	501	31.6	251	12	US-10-424-599-273602
13	486	30.7	229	12	US-10-424-599-226651
14	480	30.3	309	12	US-10-424-599-18205
15	477.5	30.2	238	12	US-10-424-599-273603

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Result No.	Score	Query Match	Length	DB ID	Description
1	722.5	45.6	354	15	US-10-388-269-2
2	627.5	39.6	358	15	US-10-409-701-5
3	621.5	39.3	358	14	US-10-320-230-12
4	620.5	39.2	358	14	US-10-320-230-12
5	613.5	38.8	323	12	US-10-425-114-38749
6	595	37.6	345	12	US-10-425-114-53407
7	595	37.6	345	12	US-10-425-114-56939
8	585.5	37.0	340	12	US-10-425-114-49308
9	563.5	35.6	344	15	US-10-310-154-411
10	554.5	35.0	390	14	US-10-320-230-12
11	521.5	32.9	356	15	US-10-310-154-430
12	501	31.6	251	12	US-10-424-599-273602
13	486	30.7	229	12	US-10-424-599-226651
14	480	30.3	309	12	US-10-424-599-18205
15	477.5	30.2	238	12	US-10-424-599-273603

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Matches 142; Conservative 59; Mismatches 74; Indels 81; Gaps 10; Db 267 LKSGASSISSVQSPICGVDAACLSQQSDDATVGSPAVCY---HSSSTS 313

Query 10 LICTESN----VDECR------IIDEPIBISIPQMG 37
Db 12 LICAEDNAATLGLDDDGEESSAAAATPPRTVYAAATGVAVDGLITEFPL----- 63

RESULT 6
US-10-425-114-53407
; Sequence 53407, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E.
; APPLICANT: Tabaska, Jack E.
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; Title of Invention: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 53407

Query 38 FSQSESEERIMENVEKEKOHLPSSDDYIKRLL-RSGDLDLNWGRDAINWIKACEVHQFG 95
Db 64 ---LSDICVATLVEREVEHMPAGEYLQKLQAVACLSLAAKIEETEVPMILQDQPF 155

Query 96 PLCFCLAMNYLDRFLSYHDLPSGKGWNLQLLAVACLSLAAKIEETEVPMILQDQPF 155
Db 120 PTAFLSTYNDLRFSLTYEPGRANMTQLAVACLSLAASKIEETVPLDQVAFAK 179

Query 156 VFEAKSVORMELLVNLKWRLLAATPCSYIRFLRKNSKCOEPSNTLISRSLOVIAST 215
Db 180 VPEGTRTIRMELVLSTKWRMHAVTACSFVEFLHKLSD-HGAPSILARSRSDDLVST 238

Query 216 TKGIDFLFLEPRPSEAAAVALVSGBLQRFHDNSFSFSPFLSLQKERVVKIGEMIE--- 271
Db 239 AKGAEVVTPRPSEAAVALVLAATVIAAGCCTSSVIERASSCKY-LDKERVLRCHMIOQEKIT 296

Query 272 -----SDGSDLICS--QTPNQVLEVSAC-----CFSFKTHDSSS 303
Db 297 MGSTVLKSAASSISSVQSPICGVDAACLSQQSDDATVGSPAVCY---HSSSTS 348

OTHER INFORMATION: Clone ID: UC-ZMFLB73363C10_FLI.pep
US-10-425-114-53407

Query Match 37.6%; Score 595; DB 12; Length 345;
Best Local Similarity 44.3%; Pred. No. 7e-54; Gaps 7;
Matches 132; Conservative 49; Mismatches 87; Indels 30; Gaps 7;

Query 1 MAEENLIEL---LICTE---SNYDDEGMIVDEPI-----EISIPQMGFSQSPEB 44
Db 54 MAPSSEYEVASILLCAEDSLLDEABEEALLARSSEPGGAEFPVP-----SE 105

Query 45 EIIMEMVEKEKOHLPSSDDYIKRLLRGDLDLNWGRDAINWIKACEVHQGPLCFCCLAMN 104
Db 106 ECVAGGLESEAAHMIPREDAEILRGMDMLRV-KTDAIDMWIKVHTCYGFGLPLAALVN 164

Query 105 YLDRRLSVIDLPSGKGWNLQLLAVACLSLAAKIEETEVPMILQDQPFVFRKSYQR 164
Db 165 YLDRRLSVIDLPSGKGWNLQLLAVACLSLAAKIEETEVPMILQDQPFVFRKSYQR 164

Query 166 MELLVNLKWRLLAATPCSYIRFLRKNSKCDOPPSNTLISRSQVIASTTRGIDFLF 224
Db 225 MELLVNLKWRMHAVTACSFVEFLHKLSD-HGAPSILARSRSDDLVSTLICIAERTHCLDF 283

Query 225 RPSEAAAAYAVLSVSGELQRFHDNSFSPLSFLSLQKERYTKKGMIESDSDLCSQTP 282
Db 284 RPSEAAAAYAVLSVSGELQRFHDNSFSPLSFLSLQKERYTKKGMIESDSDLCSQTP 282

OTHER INFORMATION: Clone ID: UC-ZMFLB73363C10_FLI.pep
US-10-425-114-38749

Query Match 38.8%; Score 613.5; DB 12; Length 323;
Best Local Similarity 45.0%; Pred. No. 7.e-56; Gaps 7;
Matches 131; Conservative 55; Mismatches 68; Indels 37; Gaps 7;

RESULT 7
US-10-425-114-56939
; Sequence 56939, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E.
; APPLICANT: Tabaska, Jack E.
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; Title of Invention: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 38749
; LENGTH: 323
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE: OTHER INFORMATION: Clone ID: UC-ZMFLB73363C10_FLI.pep
US-10-425-114-38749

Query 43 SEEITMEMVEKEKOHLPSSDDYIKRLL-RSGDLDLNWGRDAINWIKACEVHQGPLCFC 100
Db 30 SDDCVATLVEREVEHMPAGEYLQKLQAVACLSLAAKIEETEVPMILQDQPFVFEAK 160

Query 101 LAMNYLDRFLSYHDLPSGKGWNLQLLAVACLSLAAKIEETEVPMILQDQPFVFEAK 160
Db 90 LSVNVLDRFLSYEPGRANMTQLAVACLSLAASKIEETVPLDQVAKEVFEGR 149

Query 161 SVORMELVNLKWRLLAATPCSYIRFLRKNSKCDOPPSNTLISRSQVIASTTRGID 220
Db 150 TIKRMEVLVLSTKWRMHAVTACSFVEFLHKLSD-HGAPSILARSRSDDLVSTKGA 208

Query 221 FILEPRPSEAAAVALVSGBLQRFHDNSFSPLSFLSLQKERYTKKGMIESDSDLCSQTP 282
Db 209 FVVERPSTIAASTALAAAGCCTSSVIERASSCKY-LDKERVLRCHMIOQEKITAGSIY 266

Query 272 - SDGSDLICS--QTPNQVLEVSAC-----CFSFKTHDSSS 303

TYPE: PRT
 ORGANISM: Zea mays
 OTHER INFORMATION: Clone ID: 701163268_FLI.pep
 US-10-425-114-56939

Query Match Score 595; DB 12; Length 345;
 Best Local Similarity 44.3%; Pred. No. 7e-54;
 Matches 132; Conservative 49; Mismatches 87; Indels 30; Gaps 7;

Qy 1 MAENNL---LLCTE---SNVDEGMIVDETPI-----BISIPONGFQSOSBE 44
 Db 54 MAPSSYEVAASILCAEBOSSSLIDEAAEEALLARSGEPPGAEPPVP-----SE 105

RESULT 9
 US-10-310-154-411
 Sequence 411, Application US/10310154
 Publication No. US2003033670A1
 GENERAL INFORMATION:
 APPLICANT: Edgercon, Michael D
 APPLICANT: Chomet, Paul S.
 APPLICANT: Adams, Thomas H.
 APPLICANT: Ruff, Thomas G.
 APPLICANT: Agarwal, Ameeta K.
 APPLICANT: Ahrens, Jeffrey E.
 APPLICANT: Ball, James A.
 APPLICANT: Banu, G.
 APPLICANT: Bell, Erin
 APPLICANT: Bodhipalli, Raghava
 APPLICANT: Deikman, Jill
 APPLICANT: Deng, Molian
 APPLICANT: Dong, Jinzhou
 APPLICANT: Duff, Stephen M.
 APPLICANT: Galligan, Meghan M.
 APPLICANT: Hinckley, Brenda S.
 APPLICANT: Huang, Shihshieh
 APPLICANT: Johnson, G. Richard
 APPLICANT: Jung, Vincent
 APPLICANT: Kretzmer, Keith A.
 APPLICANT: Laccetti, Lucille B.
 APPLICANT: Lai, Chao-Qiang
 APPLICANT: Lee, Gary
 APPLICANT: Lin, Jie-Yi
 APPLICANT: Liu, Jingdong
 APPLICANT: Liu, Bin
 APPLICANT: Luettich, Michael M.
 APPLICANT: Lund, Adrian
 APPLICANT: Madison, Linda L.
 APPLICANT: Mailoy, Kathleen A.
 APPLICANT: McKiel, Christine L.
 APPLICANT: Miller, Phillip W.
 APPLICANT: Padmavathi, Marchikanti
 APPLICANT: Parnell, Laurence D.
 APPLICANT: Start, William G.
 APPLICANT: Tennesen, Dan
 APPLICANT: Vidya, K.R.
 APPLICANT: Xin, Zhanqiao
 APPLICANT: Yang, Chunzhi
 APPLICANT: Zhang, Xiaoping
 APPLICANT: Zhao, Yajuan
 APPLICANT: Zhou, Li
 TITL OF INVENTION: Gene Sequences and Uses Thereof in Plants
 FILE REFERENCE: 38-15(52796)B
 CURRENT APPLICATION NUMBER: US/10/310,154
 CURRENT FILING DATE: 2002-12-04
 PRIOR APPLICATION NUMBER: 60/337,358
 PRIOR FILING DATE: 2001-12-04
 NUMBER OF SEQ ID NOS: 736
 LENGTH: 340

TYPE: PRT
 ORGANISM: Zea mays
 OTHER INFORMATION: Clone ID: 700102335_FLI.pep
 US-10-425-114-49308

Query Match Score 585.5; DB 12; Length 340;
 Best Local Similarity 43.7%; Pred. No. 6.7e-53;
 Matches 135; Conservative 45; Mismatches 86; Indels 43; Gaps 8;

Qy 1 MAENNL---SILCTESNVDEGMIVD-----ETPIEISIIPQM 37
 Db 50 MAPSSYEMMASTLICGE---DSSSILDLEAGGOBEEVLLARSRTROPSVVFPPV-- 102

Qy 38 FSQSESEETIIMEMVEKERKDHPLPSDYIKHLRSGDLDIINYGRRDALNNWKAECVHQGPL 97
 Db 103 ---SEDCVAGFVEAAHMPREDYAAERLRGEGSTDLYR-RTDAIDWVWHAYYGFGL 156

Qy 98 CFCLAMNYIDRFLSWHDLSFGKGMWILQLAVACSLAKIEETEVPMILDQYGDQFV 157
 Db 157 TAACLAVNVLDRFLSYLQFEGKSHTTQLISVACSLAKMEETYVPPSLDLQYGDAYV 216

Qy 158 EAKSVQRMMLVNLKWRRAITPCSYTRYFLRIMSKDQEPSNTLIRSLSQVIASSTK 217

US-10-310-154-411
 Query Match Score 56.5%; DB 15; Length 344;
 Best Local Similarity 41.3%; Pred. No. 1.5e-50;
 Matches 133; Conservative 55; Mismatches 105; Indels 29; Gaps 8;
 Qy 9 SLLCTESNVYDEGMIIVDEPIEISIPQMGFSQ-----SESEBIMENTVEKEKOHLPD 61
 Db 11 TLLCEDRNNVGLCGNLINEVGSGHOLDNGRDALNWTKAKEYTHOFGPLCFLCLAMNYLDRELSVHDLPSGRKW 70
 Qy 62 DYIKRLRSGLDNLNGRDALNWTKAKEYTHOFGPLCFLCLAMNYLDRELSVHDLPSGRKW 121
 Db 71 GYAERLGERGLEYS WRRDAMDWICKVHSYRFGEGLSLYLVNTLDRFSSYDLPDHDKW 129
 Qy 122 ILQLIACATSLAAKIEETEVPMLEIDQVGDQFYEAKSVORMELLIJNKLYRBLAT 181
 Db 130 MRQLSVAACLAVMEEVTPLPVQCDVKFFEARTRIGMELVLATLKWRMOMATT 189
 Qy 182 PCSYIRYFLRMSKCDQEFSNTLIRSLOVTASTTRGIDLEFRSEAAAVALSVGEL 241
 Db 190 PFTFSYFLDKPFG-GKPMSKHLARCTBTIGLKGSTSPLSFRESEIAANASLAVSN 248
 Qy 242 Q-----RVHEDNSSFSPLSLCKER-VKKGEMIESGSDLCSQTENGYLEVS 289
 Db 249 QVGGSSAALSASEVPINKENIARTCYLBOALVRKTGH---NGSPSPVQSPGIVLD-- 303
 Qy 290 ACCFSFKTHD---SSSSYTHIS 308
 Db 304 ATCFSPRSDEVRLGSSQSNNIS 325

RESULT 11
 US-10-320-230-14
 / Sequence 14, Application US/10320230
 / GENERAL INFORMATION:
 / APPLICANT: Lowe, Keith S.
 / APPLICANT: Tao, Yumin
 / APPLICANT: Gordon-Kamm, William J.
 / APPLICANT: Gregory, Carolyn A.
 / APPLICANT: McElver, John A.
 / APPLICANT: Hoerster, George J.
 / TITLE OF INVENTION: Cyclin D Polynucleotides, Polypeptides
 / TITLE OF INVENTION: and Methods of Use
 / FILE REFERENCE: 092 6D
 / CURRENT APPLICATION NUMBER: US/10/320,230
 / CURRENT FILING DATE: 2002-12-16
 / PRIOR APPLICATION NUMBER: 60/101,551
 / PRIOR FILING DATE: 1998-09-23
 / PRIOR APPLICATION NUMBER: 09/398,858
 / PRIOR FILING DATE: 1999-09-20
 / NUMBER OF SEQ ID NOS: 30
 / SOFTWARE: FastSEQ for Windows Version 3.0
 / SEQ ID NO: 14
 / LENGTH: 390
 / TYPE: PRT
 / ORGANISM: Sea mays
 US-10-320-230-14

Query Match Score 554.5%; DB 14; Length 390;
 Best Local Similarity 39.1%; Pred. No. 1.6e-49;
 Matches 135; Conservative 52; Mismatches 89; Indels 69; Gaps 9;

Qy 10 LLCTESNVY---DEGMVDEPIEISIPQMGFSQ-----SESEBIMENTVEK 53
 Db 13 LILCAEEHSSILNDE---EEEFLAEVRRGRGSRSPGYGDDFGADLFPQSEPCVAGLVER 68

Qy 54 EKOLHPSPDYIKRLRGOLDNLNGRDLALNWKAECVHQGPGLCFLCLAMNYLDRELSVH 113
 Db 69 ERHMPGGCGYGDLRGGGGCLCV-RREAVDWIWKAYTHHRFRPLTAYAVNYLDRELSLS 127

Qy 114 DLPSGKGTWLLQIAVACSLAAKIEETEVPMLEIDQVGDARYFEAKTVQRMEILLVLTTL 173

Db 128 EVPDGKDWTQLLIAVACVSLAAKMEETAVPQCLDLQVGDARYFEAKTVQRMEILLVLTTL 187
 Qy 174 KWDRDAITFPCSYYTRFLRKMSK-CDQESNTLISRSQVIASTTRGIDLEFRPSEAAA 232
 Db 188 NWPRNGHATVPEFSYVDFYFLNKLNQSAELRLRARGTGCYGRPFSEIRAA 247
 Qy 233 VALSVGETQR-----VHDNSSPSPLSLILQKERVKKGEMIESGDSLQ---- 278
 Db 248 VAARAGDVFDDWENACCAYHD-----KERVLRGCBATGMASSAAIDGDA 295
 Qy 279 -----SOPNGVILEVSACCFSPKTHDSSS 303
 Db 296 TVPPKSARRRSSPVPVVPQSPVGVLD-AAACLSYRSEEAATA 339

RESULT 12
 US-10-310-154-430
 / Sequence 430, Application US/10310154
 / Publication No. US/0030233670A1
 / GENERAL INFORMATION:
 / APPLICANT: Edgerton, Michael D
 / APPLICANT: Chomet, Paul S.
 / APPLICANT: Adams, Thomas H.
 / APPLICANT: Ruff, Thomas G.
 / APPLICANT: Agarwal, Ameeta K.
 / APPLICANT: Ahrens, Jeffrey E.
 / APPLICANT: Ball, James A.
 / APPLICANT: Banu, G.
 / APPLICANT: Bodupalli, Raghava
 / APPLICANT: Bell, Erin
 / APPLICANT: Deikman, Jill
 / APPLICANT: Deng, Molian
 / APPLICANT: Dong, Jinzhuo
 / APPLICANT: Duff, Stephen M.
 / APPLICANT: Galigan, Meghan M.
 / APPLICANT: Hinckey, Brenda S.
 / APPLICANT: Huang, Shihshieh
 / APPLICANT: Johnson, G. Richard
 / APPLICANT: Jung, Vincent
 / APPLICANT: Kreitzmer, Keith A.
 / APPLICANT: Lacetti, Lucille B.
 / APPLICANT: Lai, Chao-Qiang
 / APPLICANT: Lee, Gary
 / APPLICANT: Lin, Jie-Yi
 / APPLICANT: Liu, Jingdong
 / APPLICANT: Lu, Bin
 / APPLICANT: Luechy, Michael M.
 / APPLICANT: Lund, Adrian
 / APPLICANT: Madison, Linda L.
 / APPLICANT: Malloy, Kathleen A.
 / APPLICANT: McKiel, Christine L.
 / APPLICANT: Miller, Phillip W.
 / APPLICANT: Padmavathi, Manchikanti
 / APPLICANT: Parneil, Laurence D.
 / APPLICANT: Start, William G.
 / APPLICANT: Temszen, Dan
 / APPLICANT: Vidya, K.R.
 / APPLICANT: Wang, Haiyun
 / APPLICANT: Xin, Zhanguo
 / APPLICANT: Xu, Nanfei
 / APPLICANT: Yang, Chunzhi
 / APPLICANT: Zeng, Xiaoping
 / APPLICANT: Zhang, Qiang
 / APPLICANT: Zhao, Yajuan
 / APPLICANT: Zhou, Li
 / TITLE OF INVENTION: Gene Sequences and Uses Thereof in Plants
 / FILE REFERENCE: 38-15(52796)B
 / CURRENT APPLICATION NUMBER: US/10/310,154
 / CURRENT FILING DATE: 2002-12-04
 / PRIOR APPLICATION NUMBER: 60/337,358
 / PRIOR FILING DATE: 2001-12-04
 / NUMBER OF SEQ ID NOS: 736
 / SEQ ID NO 430

;

LENGTH: 356

;

TYPE: PRT

ORGANISM: *Oryza sativa*

US-10-310-154-430

Query Match Score 521.5; DB 15; Length 356;

Best Local Similarity 44.4%; Pred. No. 4.2e-46;

Matches 119; Conservative 49; Mismatches 89; Indels 11; Gaps 6;

RESULT 13

Qy 42 ESEBEIIMMVEKEKQHLPSSDDYIKRIRSGDLDLNVRGRDAALNWIKACEVHOFGLCFCFL 101
Db 60 DSDEFVALLVEKEMDHOPQRGYLEKLELGLECS-WRKDAIDWICKYHSYNNFGPLSLYT 118 ; Sequence 226651 ; Application US/10424599
; Publication No. US20040031072A1

Qy 102 AMNYLDRFFPSVHDLPGSKGWILQOLLAVACLSLAAKIEETEVPMMLQDQFVFAKS 161 ; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J
; APPLICANT: Kovacic, David K
; APPLICANT: Zhou, Yihua

Qy 119 AVYNYLDRFFPSVHDLPGSKGWILQOLLAVACLSLAATKMEETVPLPMDQVFDAYVFEARH 178 ; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B

Qy 162 VORMELLYNKLKWLRLRATTPCSYIYFLRKNSKCDOEPNTLISRSIQLQVIASTTKCDF 221 ; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28

Db 179 IKRMELIYWKTLKWLRLQATVTPFIGFLDKNE-GREPPSYTLASWSCLTYGLTLDQRSF 237 ; SEQ ID NO: 285684
; LENGTH: 229

Qy 2222 LERPRSEAAAVAVSVGLEYRHDNSFSPLSLLQKERYKKIGEMIES-----DG 274 ; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE: NAME/KEY: unsure

Db 238 LSFRPSEAAAVAVLAVLAENQFLVE-NSALGESBIPVTKNMVRCYBLMVERALKRKIRN 296 ; OTHER INFORMATION: LOCATION: (1); OTHER INFORMATION: unsure at all Xaa locations

Qy 275 SDLCSQTNGVLEY-SACCFSEKTHDSS 301 ; OTHER INFORMATION: Clone ID: PAT_MRT3847_4669/C.1.pep

Db 297 SNASSSPVHPSPITVLDAACFSFRSDDT 324 ; OTHER INFORMATION: Best Local Similarity 47.2%; Pred. No. 1.2e-12;
; Matches 102; Conservative 36; Mismatches 46; Indels 32; Gaps 5;

RESULT 12

US-10-424-599-273602

Sequence 273602, Application US/10424599

Publication No. US20040031072A1

GENERAL INFORMATION:

APPLICANT: La Rosa, Thomas J

APPLICANT: Kovacic, David K

APPLICANT: Zhou, Yihua

APPLICANT: Cao, Yongwei

TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
FILE REFERENCE: 38-21(53223)B

CURRENT APPLICATION NUMBER: US/10/424,599

CURRENT FILING DATE: 2003-04-28

SEQ ID NO: 273602

LENGTH: 251

TYPE: PRT

ORGANISM: Glycine max

FEATURE: NAME/KEY: unsure

LOCATION: (1); (251)

OTHER INFORMATION: unsure at all Xaa locations

OTHER INFORMATION: Clone ID: PAT_MRT3847_89084C.1.pep

RESULT 14

US-10-424-599-218205

Sequence 218205, Application US/10424599

Publication No. US20040031072A1

GENERAL INFORMATION:

APPLICANT: La Rosa, Thomas J

APPLICANT: Kovacic, David K

APPLICANT: Zhou, Yihua

APPLICANT: Cao, Yongwei

TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
FILE REFERENCE: 38-21(53223)B

CURRENT APPLICATION NUMBER: US/10/424,599

CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 285684

LENGTH: 251

TYPE: PRT

ORGANISM: Glycine max

FEATURE: NAME/KEY: unsure

LOCATION: (1); (251)

OTHER INFORMATION: unsure at all Xaa locations

OTHER INFORMATION: Clone ID: PAT_MRT3847_89084C.1.pep

Qy 55 KOHLPSDDYIKRIRSGDLDLNVRGRDAALNWIKACEVHOFGLCFCFLANNYLDRFLSYH 114
Db 7 BENLQDGFLYKLISGLDLSV-RKGALDIWK-----38 ; Sequence 226651 ; Application US/10424599
; Publication No. US20040031072A1

Qy 115 LPSKGKWILQOLLAVACLSLAAKIEETEVPMMLQDQFVFAKSYH 174 ; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J
; APPLICANT: Kovacic, David K
; APPLICANT: Zhou, Yihua

Db 39 --RGKSWSMOLLAVACLSLAARMEEBKVPPCDVQFLXPKFAFKDQRMELLVLSIR 96 ; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B

Qy 175 WRLRAITPCSYIYFLRKNSKCDOEPNTLISRSIQLQVIASTTKGIDFLERPSRAAAA 234 ; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28

Db 97 WKMQASTPFSFLDFLRKIT-CDQVIVKSSILRSVGPINLKCTNFELFRPSIIAAA 155 ; NUMBER OF SEQ ID NOS: 285684

SEQ ID NO 218205

Job time : 58 secs

; LENGTH: 309
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_39067C.1.pep
US-10-424-599-218205

Query Match 30.3%; Score 480; DB 12; Length 309;
Best Local Similarity 41.5%; Pred. No. 8.2e-42;
Matches 110; Conservative 44; Mismatches 83; Indels 28; Gaps 7;

Qy 44 EETIMEMVKKEKQHLPSSDYIKRLRSQGDLIDNVRGRDNLWINKACEVHQFGPLCFCIAM 103

Db 20 EAALAGLILDEAEPHMPEKDYIIRRGRDRSVDV-TARLDAYNWILKVAHYEFPSPVTAFLSV 78

Qy 104 NYLDRFLSYVHDLP - SGKGTWILQLAVACISLAAKIEETEPMILDQVGDPOFVFEARS 161

Db 79 NYFDRFLSRCISLPPQSG - GWAQFOLISVACISLAAKMESSHVPFLDLQLEPKEVFEKT 137

Qy 162 VORMELLVNLKWKVLRLATPCSYTRYFLRK - SKCDCQEPNTLJSRSLQVIASTTKGID 220

Db 138 IQRMLWNSNLKWLRLSPVFDLHYFSLRKPSSSSQSLNHFSTSNLISSTRVN 197

Qy 221 FLERPSE-AAAAVALSVSQSELQYHEDNSFSBLFSLQKERYVKIGEMMIESDGSDLIC- 278

Db 198 FLGPAPSTVAAAVALCSANGQPLSFHD-----TIDDEMVRCCQHLMEEYVVDTCP 248

Qy 279 -----SQTPNGVILEVSAC 291

Db 249 ASIKWRITTEAAAPSSSPVGVLDAAATC 273

RESULT 15

US-10-424-599-273603

; Sequence 273603, Application US/10424599
; Publication No. US20040031072A1

GENERAL INFORMATION:

; APPLICANT: La Rosa Thomas J

; APPLICANT: Kovacic David K

; APPLICANT: Zhou Yihua

; APPLICANT: Cao Yongwei

; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With

; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

; FILE REFERENCE: 38-21.(53223)B

; CURRENT APPLICATION NUMBER: US/10/424,599

; CURRENT FILING DATE: 2003-04-28

; NUMBER OF SEQ ID NOS: 285684

; LENGTH: 238

; TYPE: PRT

; ORGANISM: Glycine max

; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_89085C.1.pep

US-10-424-599-273603

Query Match 30.2%; Score 477.5; DB 12; Length 238;
Best Local Similarity 58.6%; Pred. No. 1e-41;
Matches 92; Conservative 30; Mismatches 28; Indels 7; Gaps 3;

Qy 42 ESEETIMEMVKKEKQHLPSSDYIKRLRSQGDLIDNVRGRDNLWINKACEVHQFGPLCFCI 101

Db 89 QSDETRMGLVGRESEHLPHYGLRLLSGLDLSV-RKEFLDWIKWAHYDFGPGCSLCI 147

Qy 102 AMNYLDREFSYTHDLSGKGWLQLAVACISLAAKIEETEPMILDQVGDPOFVFEARS 161

Db 148 SVNVLDRFLSYTLEPRGKSMSQLLAVACISIAARMEETKVPPCYDLSV---QPAFEARD 202

Qy 162 VORMELLVNLKWKVLRLATPCSYTRYFLRKMSKCDQ 198

Db 203 IQRMLWNSNLKWLSPVFDLHYFSLRKPSSSSQSLNHFSTSNLISSTRVN 238

Result No.	Score	Query Match	Length	DB ID	Description
--					cyclin protein-like
1	954	60.3	317	2 T49995	cyclin D-like prot
2	660.5	41.7	372	2 T09961	probable cyclin D
3	635.5	40.1	361	2 S84613	cyclin delta-2 - A
4	633.3	40.0	383	2 S51651	hypothetical prote
5	434.5	28.0	339	2 A96725	cyclin delta-1 - A
6	434	27.4	334	2 S51650	cyclin delta-3 - A
7	392	24.8	376	2 T05420	cyclin 4, D-type -
8	354.5	22.4	386	2 T09598	cyclin D-like pro
9	353	22.3	361	2 T45860	probable D-type cy
10	305	19.3	302	2 E85041	hypothetical prote
11	265.5	16.8	321	2 T04720	cyclin D1 - Africa
12	260.5	16.5	291	2 S57922	cyclin D1 - zebra
13	253	16.0	562730		cyclin D2 - rat
14	242	15.3	288	2 T58372	cyclin D2 - mouse
15	241	15.2	289	2 A41984	cyclin D1 - mouse
16	239	15.1	295	2 A56523	cyclin D1 - human
17	236	14.9	295	2 A88977	cyclin D1 - rat
18	235	14.8	295	2 JC2342	cyclin D2 - human
19	232	14.7	289	2 A42822	cyclin D2 - rat
20	231	14.6	288	2 JC4011	cyclin D2 - chicken
21	224.5	14.2	291	2 JC4579	cyclin D2 - Africa
22	220.5	13.9	291	2 SS7925	cyclin A-like Prot
23	216.5	13.7	502	2 T02746	cyclin II - maize
24	204.5	12.9	456	2 C57742	probable mitotic c
25	198	12.5	454	2 A96803	cyclin E - human
26	188.5	11.9	395	2 A40270	cyclin A-type - C
27	187.5	11.8	493	2 T03609	cyclin A-type (C)
28	181.5	11.5	482	2 T02967	cyclin D3 - human
29	181	11.4	292	2 H42822	

Copyright (c) 1993 - 2004 Compugen Ltd.
 OM protein - protein search, using SW model
 Run on: March 23, 2004, 16:35:16 ; Search time 26 Seconds
 (without alignments)
 1139.500 Million cell updates/sec
 Title: US-09-530-209A-2
 Perfect score: 1583
 Sequence: 1 MABENIELSLCTESNVDDE.....SACCFSFKTHDSSSYTHLS 308
 Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5
 Searched: 283366 seqs, 9619526 residues
 Total number of hits satisfying chosen parameters: 283366

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

RESULT 1
 T49995
 cyclin protein-like - Arabidopsis thaliana
 N;Alternate names: Protein F12B17.210
 C;Species: Arabidopsis thaliana (mouse-ear cress)
 C;Date: 02-Jun-2000 #sequence_revision 02-Jun-2000
 C;Accession: T49935
 R;Bayan, M.; Bancroft, I.; Mewes, H.W.; Rudd, S.; Lemcke, K.; Mayer, K.F.X.
 submitted to the Protein Sequence Database, April 2000
 A;Reference number: Z25026
 A;Map position: 5
 A;Status: Preliminary
 A;Molecule type: DNA
 A;Residues: 1-317 <BEV>
 A;Cross-references: EMBL:AL353995; GSPDB:GN00063; ATSP:F12B17.210
 A;Experimental source: cultivar Columbia; BAC clone F12B17
 C;Genetics:
 A;Gene: ATSP:F12B17.210
 A;Accession: T49935
 A;Introns: 78/3; 107/3; 140/3; 221/3; 265/3

RESULT 1
 T49995
 cyclin protein-like - Arabidopsis thaliana
 N;Alternate names: Protein F12B17.210
 C;Species: Arabidopsis thaliana (mouse-ear cress)
 C;Date: 02-Jun-2000 #sequence_revision 02-Jun-2000
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 R;Bayan, M.; Bancroft, I.; Mewes, H.W.; Rudd, S.; Lemcke, K.; Mayer, K.F.X.
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 A;Reference number: Z25026
 A;Map position: 5
 A;Status: Preliminary
 A;Molecule type: DNA
 A;Residues: 1-317 <BEV>
 A;Cross-references: EMBL:AL353995; GSPDB:GN00063; ATSP:F12B17.210
 A;Experimental source: cultivar Columbia; BAC clone F12B17
 C;Genetics:
 A;Gene: ATSP:F12B17.210
 A;Accession: T49935
 A;Introns: 78/3; 107/3; 140/3; 221/3; 265/3
 Query Match 60.3%; Score 954; DB 2; Length 317;
 Best Local Similarity 64.8%; Pred. No. 1.e-71
 Matches 212; Conservative 23; MisMatches 58; Indels 8; Gaps 8,
 Qy 4 ENELPLLCETESNDYDEGMIVDTPIEISITPONGFSQSESEEITIMEKEKOHPSDDY 63
 Db 3 EFMEPNLV -- SNEFDEKSNSVUDTR -- SIRQNGF - PLEASEEIVREMTKEKOHPSRDDY 55
 Qy 64 IKRLRSGLDLNLYGRDAINWIKACEYHQFGPLICFLCCLAMNYLDRFLSYHDIPSGKGWNTL 123
 Db 56 LKRJRNDDDFNV-RIQAGGWINKACEELQFGPLCILAMNYLDRFLSYHDIPSGKAVTY 114
 Qy 124 QLLAVACLSLAAKIEETEVPMILDQGDPQFYREAKSVORMELLUNNLKLRKRAITTPC 183
 Db 115 QLLAVACLSLAAKIEETVPEMLQOLOGQAPMFTEAKSVORMELLVNVLNRBLRATPC 174
 Qy 184 SYRYFLRKMSKCDQEPNTLISRSLOVIASTTK---GIDFLBF 224
 Db 175 SYRYFLSKINGDQEPNSRLVTRSLQVIASTYKGDGLLFFKGVLIVDVAGIDLF 234
 Qy 225 RPSEAAAVAVALSYSGEVHFDNSSSPLFSSLQERVKCIGEMTSGDSLICSOFPNG 284
 Db 235 RASEIAAAVALSYSGEVHFDNSSSPLFSSLQERVKCIGEMTSGDSLICSOFPNG 290
 Qy 285 -VLEVSACCP--SFKTDHSSSYTHLS 308
 Db 291 TVLQFSRYSRSHLSAVSSSSTLS 317
 RESULT 2
 T03961

cyclin D-like protein - red goosefoot
 C;Species: Chenopodium rubrum (red goosefoot)
 C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 16-Jul-1999
 C;Accession: T09961
 R;Renz, A.; Fountain, M.; Beck, E.
 submitted to the EMBL Data Library, December 1996
 A;Description: Nucleotide sequence of a cDNA encoding a D-type cyclin from a photoautotrophic plant
 A;Reference number: Z16906
 A;Accession: T09961
 A;Status: preliminary; translated from GB/EMBL/DDBJ
 A;Molecule type: mRNA
 A;Residues: 1-372 <REN>
 A;Cross-references: EMBL:Y10162; NID:e014005; PID:e290219
 A;Experimental source: 7 day old culture; photoautotrophic cells derived from hypocotyl
 C;Genetics:
 A;Gene: cyclin D-like protein
 C;Keywords: cell cycle control; cell division control
 Query Match 41.7%; Score 660.5; DB 2; Length 372;
 Best Local Similarity 44.1%; Pred. No. 4 1e-49;
 Matches 150; Conservative 63; Mismatches 76; Indels 51; Gaps 10;
 Qy 10 LLCTEEN-----VDDDEGM-LVDEDTPEIESTIPQM----- 36
 Db 7 LLAEDNSSSIDEVDNNYYGVDDDDYQCNLQQCQGNLNRLNEDDFLTLLIIKHNFEA 66
 RESULT 4
 S51651
 Cyclin delta-2 - Arabidopsis thaliana
 N;Alternate names: cyclin D homolog
 C;Species: Arabidopsis thaliana (mouse-ear cress)
 C;Date: 07-May-1995 #sequence_revision 21-Jul-1997
 C;Accession: S51651
 R;Sonni, R.; Carmichael, J.P.; Shah, Z.H.; Murray, J.A.H.
 D;Submitted to the EMBL Data Library, December 1994
 A;Description: A family of cyclin D homologs from plants differentially controlled by g1
 A;Reference number: S51650
 A;Accession: S51651
 A;Molecule type: mRNA
 A;Residue: 1-383 <SON>
 A;Cross-References: EMBL:X83370
 C;Keywords: cell cycle control; cell division control
 Query Match 40.0%; Score 633; DB 2; Length 383;
 Best Local Similarity 47.7%; Pred. No. 1e-46;
 Matches 144; Conservative 53; Mismatches 67; Indels 38; Gaps 9;
 Qy 32 SIPONQFSQSE-SEIIIMENVEKEQHLSDDYIKRILRGDDLNNGRDALNIWKAACEHQ 90
 Db 51 SIPPNCGSSSSSLSEDRIKEMLVRETEFCPTGTDYVRLISGCDLDSV-RNQALDWTLKVCA 109
 Qy 91 VHQFGELCPCLAMNYLDRFLSVHDLPSKGWILQLAYACLSAAKIEETEPMLIDLVQDP 153
 Db 125 FGPLCYTSLSNVYLDRELSAYELP-GKAWMQLGIVAKKUDTEPVFLDQVES 183
 Qy 154 QFVFEAKRSVORMELLYVNLKLRRAATTPCSYTRFLRMSKCDOPSNTLISSLQVIA 213
 Db 184 KVFVFEAKTIQRMELLVLSTLKWRMQSYTVPSEIDFLYKLKG-DKMPSKSLSIFQATQLIL 242
 Qy 214 STTKGIDDFLEFRPSEAAAANAVSUGELQRTFHDSSESPFLSLLQKERYVKIGEMI-- 270
 Db 243 STIKGIDLMFRPSETAAAVASVTOOTQTEFTDRAFTSFIDVKEKIRLMKCVBIMHDIL 302
 Qy 271 ---ESDG--- SDLCSCOTPNQGLEVSACCCFSRKHDSSS 303
 Db 303 RMSSRSNGALASTSVQSPGIVDASA-CSYKSDDSTP 341
 RESULT 3
 C84613
 probable cyclin D [imported] - Arabidopsis thaliana
 C;Species: Arabidopsis thaliana (mouse-ear cress)
 C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
 R;Lin, X.; Kaul, S.; Rounseley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
 M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vanaken, S.E.; Umayam, L.; Tallon, L.;
 eusis, D.; Niemann, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.
 Nature 402, 761-768, 1999
 A;Title: Sequence and analysis of chromosome 2 of the plant *Arabidopsis* thaliana.
 A;Reference number: A84420; PMID:10617197
 A;Accession: C84613
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-361 <STR>
 C;Cross-references: GB:AE002093; NID:9454444; PIDN:AAD22352.1; GSPDB:GN00139
 A;Gene: Atg22490
 A;Map position: 2
 Query Match 40.1%; Score 635.5; DB 2; Length 361;
 Best Local Similarity 42.8%; Pred. No. 5 7e-41;
 Matches 154; Conservative 58; Mismatches 75; Indels 73; Gaps 12;
 Qy 269 MIES-----DGSDLICSQ-----TPNGTLEVSACCCFSRKHDSSS 301
 Db 285 LMRSLTGEENVRGTSILSQDARVARAVAPASPGVLE-ATCLSYRSBERTVBSCTNSSQ 342
 Qy 302 SS 303
 Db 343 SS 344
 RESULT 5
 A96725
 hypothetical protein F20P5.7 [imported] - *Arabidopsis thaliana*
 SI 33

C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Fedderspiel, N.A.; Kaul, S.; White, O.; Alonso, J.; Chung, M.K.; Conn, L.; Conway, A.B.; Creasy, A.R.; Dewar, K.; Chin, C.W.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.; Rizzo, M.; Rooney, T.; Liu, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marzali, A.; Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Talion, A.; Wu, D.; Yu, G.; Fraser, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; PMID:11130712
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-334 <STO>
A;Cross-references: GB:AE005173; NID:g2194121; PIDN:AAB61096.1; GSPDB:GN00141
A;Genetics:
A;Map position: 1

Query Match 28.0%; Score 443.5; DB 2; Length 339;
Best Local Similarity 37.0%; Prod. No. 1..8e-30; Indels 41; Gaps 11;
Matches 117; Conservative 53; Mismatches 105; Result 7
Db 19 DMDLFCGE----DSGVFSGESTVD----ESSEVDSWPGDSIACFIELDERHFPFGHD 67

Qy 7 ELSLCLCTENVDDEGMIVDEPIEISIPONGFSQSESE---EIIEMMVEKEKOHLPSSDD 62
Db 19 DMDLFCGE----DSGVFSGESTVD----ESSEVDSWPGDSIACFIELDERHFPFGHD 67

Qy 63 YIKRLRGSDLDLNVRGRDANLNIWKAECVHQGPLCFLANNYLDREFLVSVDLPSGKWI 122
Db 68 YLSRFQTSRSLDA-ARESVAWLKVQAYINFPLTAVNMDFRAYARLPETSGWP 126

Qy 123 LOLIHAVCLSLAAKIEEDEVPMILQDQFVFEAKSVORMELLYVNLKWKRLRAITP 182
Db 127 MQLIHAVCLSLAAKMEETLVLPSLFDQFQAVKVLFREAKTICKMELLYVSLVDLRLRSVTP 186

Qy 183 CSYIRYFLRKMSKCDQBSNT---LISRSLOVIASTTKIDPFLFRPSEAAAVALSV 238
Db 187 FDFISFFAYKI---DGSFTFLGGFFETTILSNKEASLEYNPESTSAAAICVA 241

Qy 239 GELORVHPDNNFSFSPLFSH-----LOKERVKKGEMIES--DGSDLCSQTENGV-LE 287
Db 242 NEPLSL---SSVNPHESSETWCGLSKERIVCYRLMKAMAENRLL-NTPKVIAKLR 296

Qy 288 VSACCCFSFKTHDSSSS 303
Db 297 VSVRASSTLTRPSPDES 312

RESULT 6
S51650 cyclin delta-1 - Arabidopsis thaliana
C;Species: cyclin D homolog
C;Date: 07-May-1995 #sequence_revision 21-Jul-1995 #text_change 09-Sep-1997
R;Soni, R.; Carmichael, J.P.; Shah, Z.H.; Murray, J.A.H.
submitted to the EMBL Data Library, December 1994
A;Description: A family of cyclin D homologs from plants differentially controlled by 91
A;Accession number: S51650
A;Molecule type: mRNA
A;Residues: 1-287, 'C', 289-370, 'R', 372-376 <SON>
A;Cross references: EMBL:X83371; NID:g603508; PID:9603509
C;Keywords: C.Genetics;
A;Introns: 158/3; 226/1; 269/3
A;Note: F28n23 80
C;Keywords: cell cycle control; cell division control

Query Match 24.8%; Score 392; DB 2; Length 376;
Best Local Similarity 31.9%; Pred. No. 5..6e-26;
Matches 104; Conservative 60; Mismatches 92; Indels 70; Gaps 10;

Qy 9 SLLCTESNVDEGMIVDEPIEISIPONGFSQSESE--ESEBIMMVEKEKOHLPSSDDY 63
Db 21 ALYCEEEKWDDGSEBEENSSLSSSSPFVWVQQDLFWDEDLVTLFSKEEQGLSCLD- 79

Qy 64 IKRLRGSDLDLNVRGRDANLNIWKAECVHQGPLCFLANNYLDREFLVSVDLPSGKWI 123
Db 80 ----DVLSDTRKEAVGWLRLVNAHYGFTSLAVALITYLDKFICSYSLQRDPWML 132

Qy 124 QLLAVACSLAAKIEEDEVPMILQDQFVFEAKSVORMELLYVNLKWKRLRAITPC 183
Db 133 QINVSACSLAAKVEETQPLLDFQVEETKIVFEATQRMELLUSTLVEKMHLLTP1 192

Query Match 27.4%; Score 434; DB 2; Length 334;
Best Local Similarity 37.2%; Pred. No. 1..2e-29;
Matches 116; Conservative 52; Mismatches 110; Indels 34; Gaps 10;

Qy 184 SYIRYFLRK-----MSKCDQEPNSNTLISRLOVIASTTKGIDFLEERPSEAAA 232
Db 193 SFVDHIIIRGLKRNNAHDFLANKH-----RLLSVISDSRFVGYPSTVYAA 240

C:Species: Rattus norvegicus (Norway rat)
 C:Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 16-Jul-1999
 C:Hanna, Z.; Jankowski, M.; Tremblay, P.; Jiang, X.M.; Milatovich, A.; Francke, U.; Joli
 Oncogene 8, 1661-1666, 1993
 A;Title: The VINI gene, identified by provirus insertional mutagenesis, is the cyclin D2
 A;Reference number: 158372; PMID:93275661;
 A;Accession: 15B312;
 A;Status: preliminary; translated from GB/EMBL/DDBJ
 A;Molecule type: mRNA
 A;Residues: 1-288 <RES>
 A;Cross-references: GB:L09752; NID:g203703; PID:AAA41010.1; PMID:g203704
 C;Genetics:
 A;Gene: VINI
 C;Keywords: cyclin
 C;Keywords: cell cycle control

Query Match 15.3%; Score 242; DB 2; Length 288;
 Best Local Similarity 29.0%; Pred. No. 3.3e-13;
 Matches 88; Conservative 51; Mismatches 124; Indels 40; Gaps 14;

Qy 8 LSLLCTESNVDEGMIVDTPIETSIQNGFSQSSEBTIMENVEKEVKOHLPPDDYTKRL 67
 Db 1 MELLCCCE-----VD--PVRAVDPDRNLE--DRVQNLTILTERRYLPCSYKCV 46

Qy 68 RSGDLDLNVGRDALLNIWKAECVHQFGLCFLAMMYDLRFLSPGKWIQLLA 127
 Db 47 QK-DIQPM-RKAVATWMJVECEQKCEEVFPAMNTLDRFLA-GVPTPKTH-LQLG 101

Qy 128 VACLSLAAKIEETEVPMILDLQVGDQFYFEAKSVORMELL----VNLKIKWRLRALT 182
 Db 102 AVCMFLASKLKT-IPL----TAEKLCIYTDSVQEELWVLGKWKNLAAVTP 155

Qy 183 CSYTRYFLRKMSKDQEPANTLISRSQV-IASTTKGIDFLERPSE AAAVALVSGB 240
 Db 156 HDFTIELFLRKLPQ--QKEKLSLIRKAQTFFIALCATDFKAMYPPSMIAATGSVGAICGL 213

Qy 241 LQRVHFDNSSFSPLESQFLSPLFSLQK----BRVKIGEMES 272
 Db 214 QQDEVVNAHTCDALTELLAKHTDVLCKACQEEA 251

Search completed: March 23, 2004, 16:39:40
 Job time : 27 secs

A;Cross-references: GB:M86182
 C;Superfamily: Cyclin
 C;Keywords: cell cycle control

Query Match 15.2%; Score 241; DB 2; Length 289;
 Best Local Similarity 29.9%; Pred. No. 4.1e-13;
 Matches 83; Conservative 50; Mismatches 105; Indels 40; Gaps 14;

Qy 8 LSLLCTESNVDEGMIVDTPIETSIQNGFSQSSEBTIMENVEKEVKOHLPPDDYTKRL 67
 Db 1 MELLCCCE-----VD--PVRAVDPDRNLE--DRVQNLTILTERRYLPCSYKCV 46

Qy 68 RSGDLDLNVGRDALLNIWKAECVHQFGLCFLAMMYDLRFLSPGKWIQLLA 127
 Db 47 QK-DIQPM-RKAVATWMJVECEQKCEEVFPAMNTLDRFLA-GVPTPKTH-LQLG 101

Qy 128 VACLSLAAKIEETEVPMILDLQVGDQFYFEAKSVORMELL----VNLKIKWRLRALT 182
 Db 102 AVCMFLASKLKT-IPL----TAEKLCIYTDSVQEELWVLGKWKNLAAVTP 155

Qy 183 CSYTRYFLRKMSKDQEPANTLISRSQV-IASTTKGIDFLERPSE AAAVALVSGB 240
 Db 156 HDFTIELFLRKLPQ--QKEKLSLIRKAQTFFIALCATDFKAMYPPSMIAATGSVGAICGL 213

Qy 241 LQRVHFDNSSFSPLESQFLSPLFSLQK----BRVKIGEMES 272
 Db 214 QQDEVVNAHTCDALTELLAKHTDVLCKACQEEA 251

RESULT 15

A41984
 Cyclin D2 - mouse
 N;Alternate names: cyclin-like protein Cy12
 C;Species: Mus musculus (house mouse)
 C;Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 16-Jul-1999
 C;Accession: A41984; B0035
 R;Kiyokawa, H.; Busque, X.; Powell, C.T.; Ngo, L.; Rifkind, R.A.; Marks, P.A.
 Proc. Natl. Acad. Sci. U. S. A. 89, 2444-2447, 1992
 A;Title: Cloning of a D-type cyclin from murine erythroleukemia cells.
 A;Reference number: A41984; MUID:92196134; PMID:137245
 A;Accession: A41984
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-289 <KIV>
 A;Cross-references: GB:M83749; NID:g192938; PID:AAA37519.1; PMID:g192939
 A;Experimental source: erythroleukemia cell^b
 A;Note: sequence inconsistent with the nucleotide translation
 A;Note: sequence extracted from NCBI backbone (NCBIN88492, NCBIPI:08493)
 R;Natsubame, H.; Roussel, M.F.; Ashmun, R.A.; Sherr, C.J.
 Cell 65, 701-713, 1991
 A;Title: Colony-stimulating factor 1 regulates novel cyclins during the G1 phase of the
 A;Reference number: A40035; MUID:9123305; PMID:1827757
 A;Accession: B40035
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 54-289 <MAT>

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OM protein - protein search, using sw model

Run on: March 23, 2004, 16:31:10 ; search time 18 Seconds
 890.978 Million cell updates/sec

Title: US-09-530-209A-2

Perfect score: 1583

Sequence: 1 MAEENDELSLCTESNVDDE.....SACCFSFKTHDSSSYTHLS 308

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Swissprot_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB	ID	Description
1	635.5	40.1	361	1	CGD2_ARATH	P42752_arabidopsis	P42752_arabidopsis
2	443.5	28.0	335	1	CGD1_ARATH	P42753_arabidopsis	P42753_arabidopsis
3	398	25.1	376	1	CGD3_ARATH	P5075 xenopus lae	P5075 xenopus lae
4	260.5	16.5	291	1	CGD1_XENLA	Q90459 brachydanio	Q90459 brachydanio
5	253	16.0	291	1	CGD1_BRARE	P50516 gallus gall	P50516 gallus gall
6	244.5	15.4	292	1	CGD1_CHICK	Q04827 rattus norv	P30247 rattus norv
7	242	15.3	288	1	CGD2_RAT	P25322 mus musculu	P25322 mus musculu
8	24	15.2	289	1	CGD2_MOUSE	P24395 homo sapien	P24395 homo sapien
9	23.9	15.1	295	1	CGD1_HUMAN	P39948 rattus norv	P39948 rattus norv
10	23.6	14.9	295	1	CGD1_HUMAN	P30279 homo sapien	P49706 gallus gall
11	23.5	14.8	295	1	CGD1_RAT	P53782 xenopus lae	P53782 xenopus lae
12	23.2	14.7	289	1	CGD2_HUMAN	P24864 homo sapien	P24864 homo sapien
13	22.4.5	14.2	291	1	CGD2_CHICK	O96020 homo sapien	P30241 homo sapien
14	22.0.5	13.9	291	1	CGD1_XENLA	Q91280 xenopus lae	Q91280 xenopus lae
15	18.8.5	11.9	410	1	CGE1_HUMAN	P30248 homo sapien	P30248 homo sapien
16	18.2	11.5	404	1	CGE2_HUMAN	P30249 medicago ba	P30249 medicago ba
17	18.1	11.4	292	1	CGD3_HUMAN	Q92238 mus musculu	P32943 secharomy
18	17.6	11.1	404	1	CGE2_MOUSE	P24861 patella vul	P24861 patella vul
19	17.5	11.1	426	1	CG2A_PATVU	P30242 mus musculu	P30242 mus musculu
20	17.3	10.9	292	1	CGD3_MOUSE	P48961 rattus norv	P48961 rattus norv
21	17.3	10.9	293	1	CGD3 RAT	P61466 mus musculu	P61466 mus musculu
22	17.2.5	10.9	421	1	CGA1_MOUSE	P46277 medicago va	P46277 medicago va
23	17.1	10.8	428	1	CGC1_MOUSE	P78396 homo sapien	P39949 rattus norv
24	17.0	10.7	465	1	CGA1_HUMAN	P30249 rattus norv	P30249 rattus norv
25	169.5	10.7	396	1	CGE1 RAT	P30248 homo sapien	P30248 homo sapien
26	168.5	10.6	406	1	CGA2_BOVIN	P30247 medicago ba	P30247 medicago ba
27	167.5	10.6	432	1	CGE2_HUMAN	P30246 homo sapien	P30246 homo sapien
28	167	10.5	328	1	CG2B_MEDSA	P32943 secharomy	P32943 secharomy
29	167	10.5	380	1	CGS6 YEAST	P5075 xenopus lae	P5075 xenopus lae
30	165.5	10.5	408	1	CGE2_XENLA	Q91280 xenopus lae	Q91280 xenopus lae
31	165.5	10.5	408	1	CGE2_MOUSE	P51943 mus musculu	P51943 mus musculu
32	164.5	10.4	422	1	CGA2_MOUSE	P49794 brachydanio	P49794 brachydanio
33	164	10.4	410	1	CGE1_BRARE		

ALIGNMENTS

RESULT 1

CGD2_ARATH

STANDARD;

PRT; 361 AA.

AC P42752;

DT 01-NOV-1995 (Rel. 32, Created)

DT 15-DEC-1998 (Rel. 37, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DB Cyclin delta-2.

GN CYCD2 OR At2g2490 OR F14M13.11.

OS Arabidopsis thaliana (Mouse-ear cress).

Eukaryota; Viridiplantae; Streptophytina; Embryophyta; Tracheophyta;

spermatophyte; Magnoliophyta; eudicotyledons; core eudicots; rosids;

euroids II; Brassicales; Brassicaceae; Arabidopsis.

NCBI TaxID=3702;

OX RN [1]

SEQUENCE FROM N.A.

RC STRAIN=CV_Landsberg erecta; TISSUE=Seedling;

RX MEDLINE=95210930; PubMed=7616881;

RX Soni R.; Carmichael J.-P.; Shah Z.H.; Murray J.A.H.;

RA "A family of cyclin D homologs from plants differentially controlled

by growth regulators and containing the conserved retinoblastoma

protein interaction motif.";

RA Plant Cell 7:85-103 (1995).

[2]

RP SEQUENCE FROM N.A.

RC STRAIN=CV_Columbia;

RX MEDLINE=95083487; PubMed=10617197;

RA Lin X.; Kaul S.; Rounseley S.D.; Shea T.P.; Benito M.-I.; Town C.D.;

RA Mason T.M.; Bowman C.L.; Barnstead M.B.; Fieldlyum T.V.,

RA Fujii C.Y.; Gill J.J.; Adams M.D.; Ketchum K.A.; Lee J.-J.; Ronning C.M.;

RA Buell C.R.; Gill J.E.; Adans A.J.; Carrera A.J.; Creasy T.H.,

RA Talton L.J.; Gill J.B.; Goodman H.M.; Somerville C.R.; Copenhaver G.P.; Preuss D.,

RA Nieman W.C.; White O.; Eisen J.A.; Salzberg S.L.; Fraser C.M.,

RA Venter J.C.;

RA "Sequence and analysis of chromosome 2 of the plant Arabidopsis

RT thaliana";

RT Nature 402:761-766 (1999).

CC -1- SIMILARITY: Belongs to the cyclin family. Cyclin D subfamily.

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CC EMBL; X63370; CAA88286.1; -.

DR DR EMBL; AC006592; ARD22352.1; -.

DR PIR; CB4613; C84613; InterPro; IPR006670; Cyclin.

DR	InterPro; IPR004367; Cyclin_Cterm.	DR	Feldblum T.V., Feng J.-D., Fong B., Fujii C.Y., Huisz L., Nieman W.C., Osborne B.I., Rowley D., Sibthorpe J., Souza M.J., Walker M., Zarzali A.
RA	Pfam; PF00134; cyclin_1.	RA	Gill J.E., Goldsmith A.D., Haas B., Hansen N.F., Hughes C., Khan S., Khaykin E., Kim C.J., Koo H.L., Johnson-Hopson C., Kurtz D.B., Lam B., Langin-Hooper S., Lee J.M., Li J.H., Li Y.-P., Liu X., Liu S.X., Luu Z.A., Luros J.S., Maiti R., Marziali A., Militscher J., Miranda M., Nguyen M., Nieman W.C., Osborne B.I., Pai G., Peterson J., Pham P.K., Rizzo M., Rooney T., Rowley D., Saito H., Salzberg S.L., Schwartz J.R., Shinin P., Southwick A.M., Sun H., Tallon L.J., Tambangua G., Toriumi M.J., Town C.D., Utterback T., Van Aken S., Vaysberg M., Vayskaya V.S., Walker M., Wu D., Yu G., Fraser C.M., Venter J.C., Davis R.W./"Sequence and analysis of chromosome 1 of the plant Arabidopsis thalianae.", Nature 408:816-820(2000).
RA	PROSITE; PS00232; CYCLINS_1.	RA	Miltzschner J., Mizanda M., Nguyen M., Nieman W.C., Osborne B.I., Pham P.K., Rizzo M., Rooney T., Rowley D., Saito H., Salzberg S.L., Schwartz J.R., Shinin P., Southwick A.M., Sun H., Tallon L.J., Tambangua G., Toriumi M.J., Town C.D., Utterback T., Van Aken S., Vaysberg M., Vayskaya V.S., Walker M., Wu D., Yu G., Fraser C.M., Venter J.C., Davis R.W./"Sequence and analysis of chromosome 1 of the plant Arabidopsis thalianae.", Nature 408:816-820(2000).
RA	PROSITE; PS00232; CYCLINS_1.	CC	-!- SIMILARITY: Belongs to the cyclin family. Cyclin D subfamily.
RA	SEQUENCE 361 AA;	CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).
RA	Query Match Score 635.5; DB 1; Length 361;	CC	RT "Sequence and analysis of chromosome 1 of the plant Arabidopsis thalianae.", Nature 408:816-820(2000).
RA	Best Local Similarity 42.8%; Pred. No. 4.2e-46;	CC	RT
RA	Matches 154; Conservative 58; Mismatches 75; Gaps 12;	CC	RT
QY	1 MAEENDLSSLTESNVDDGEMIVDEPIE-----SI 33	CC	RT
Db	1 MAE----NLAGETS---ESWIDNDDDINYGGGFTNEIDYNHOLFADKDNFGGNGSI 52	CC	RT
QY	34 POMGFSESO-SSEIIMMEMVEKERQHLPLSDDYIKRLRSGLDLDINGRDALLNTWKACEVH 92	CC	RT
Db	53 PMMGSSSSSISLSDRIKEMLVRLEFCPTDTYKLISLSDLAVS-RHQALDWLWLKVCAHY 111	CC	RT
QY	93 QFGPUCFLCLANYLDRFLPSVHDLPGKGWILQLLAVALCLSAAKIEETEVPMILIDLOYGD 152.	CC	RT
Db	112 HFGHLCCLCSCLANYLDRFLPSVHDLPGKDQDWAQQLAVALSLASKMEEDVPHFLDLOVED 171	CC	RT
QY	153 POFVFAEKPSVQRMELLYLNKLKORLRAATTPCSYTRYFLRMSKCDQEPSNTLIRSLOVI 212	CC	RT
Db	172 EKFVFEXKTIGEMLLVYVTNLWRLQALTFPSFIDYFDKIS--GHVSENLYRSSLRFI 228	CC	RT
QY	213 ASTTKGIDFLERPSE- AAAVALS/SGELQRVHFDSNSFSPLSLLQKERVKKIGEMI 270	CC	RT
Db	229 INTTKATEFLDRPSETAAAAAVSVSISGETECIDEEKALASLILY-VVKQERYKRCUNLM 286	CC	RT
QY	271 ES-----DGSDLCSQ-----TPNGYLEVSAACPSFK-----THDSSS 303	CC	RT
Db	287 RSLTGEEVNRTGTSLSQEVARAVRAPSPVGYLE--ATCILSRSEERTVECTNSSS 344	CC	RT
RESULT 2	cycl_arath	Query Match Score 443.5; DB 1; Length 335;	
ID	CGDI_ARATH STANDARD; PRT; 335 AA.	Best Local Similarity 37.0%; Pred. No. 5.6e-30; Mismatches 117; Conservative 53; MisMatches 105; Indel_B 41; Gaps 11;	
AC	P42751; O04525;	Matches 117; Conservative 53; MisMatches 105; Indel_B 41; Gaps 11;	
DT	01-NOV-1995 (Rel. 3.2, Created)	7 ELSLICTESYNDDEGMIVDEPIEISIPIQMGFSQSESE---EIIEMEMVEKEQHLPSSDD 62	
DT	15-DEC-1998 (Rel. 3.7, Last sequence update)	19 DMDFLGCE---DGSWFGSGETVD-----FSSSSVDSNFGDSTACFIEDRHFPGHD 67	
DT	28-FEB-2003 (Rel. 4.1, Last annotation update)	63 YIKRLRSGDLDLNVRGRDAINWIKVACEVHQFGPLFCCLANNYLDRFLSYDLSKGKWI 122	
DB	CYC1D OR ATIG70210 OR F20P5_7.	68 YLSRQRISLDA-AREDSWAWLKVQAYINQPLTAYLNMYDRFLPESGWP 126	
GN	OS Arabidopsis thaliana (Mouse-ear cress).	123 IQLIAYACLSAAKTEETEPVMLIDIQVGDQFQVFKYLFPAKTIKRMEJJLVLSVLWRSLVTP 182	
OS	Eukaryota; Viridiplantae; Streptophytina; Embryophyta; Tracheophyta; Spermatophytina; Magnoliophyta; eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.	127 MQLIAYACLSAAKNEEILVPLSFLDFQVAGVYKLFPAKTIKRMEJJLVLSVLWRSLVTP 186	
RN	[1]	QY	183 CSYIRYFLRMSKCDQEPSNT---LISRSLOVIASTTKGIDFLERPSEAAAVLVS 238
RP	SEQUENCE FROM N.A. STRAIN=cv. Columbia; TISSUE=Seedling; MEDLINE=952.0930; PubMed=7696881; Soni R., Carmichael J.P., Shah Z.H., Murray J.A.H.; RA Theologis A., Ecker J.R., Palm C.J., Fedderspiel N.A., Kaul S., White O., Alonso J., Altafi H., Araujo R., Bowman C.L., Brooks S.Y., Buehler E., Chan H., Chao E., Cheuk R.P., Chin C.W., Chung M.K., Conn J., Conway A.R., Creasy T.H., Dewar K., DT 01-NOV-1995 (Rel. 3.2, Created)	187 EDFISFEAYKI---DPSGCFGLGFFISHATEILSNIKEASFELTWPSSTAAAIICVA 241	
RX	RA	QY	189 GELQRVFKKIGMIES--DGGDLCSQTPENGY--LE 287
RX	RA	DB	242 NELPSI---SSVNNPHESPETWDGJLSKEKVRVCRYRLMKAMAIENNRL--NTPKVJAKLR 296
RX	RA	QY	288 VSACCFSEKTHDSSS 303
RX	RA	DB	297 VSVRASTLTPSDES 312
RESULT 3	cgdi_arath	SEQUENCE FROM N.A.	
RC	STRAIN=cv. Columbia; MEDLINE=21016719; PubMed=11130712;	CGD3_ARATH STANDARD; PRT; 376 AA.	
RC	RA	CGD3_ARATH ID CGD3_ARATH AC P42753; O4989 AC	
RA	RA	RA	

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DR EMBL: X83371; CAA50287; 1.; -.
 DR EMBL: AL01961; CAA17556; 1; -.
 DR EMBL: AL161584; CABE0133; 1; -.
 DR PIR; T05420; T05420.
 DR InterPro; IPR06670; Cyclin.
 DR InterPro; IPR043367; Cyclin_Cterm.
 DR InterPro; IPR066721; Cyclin_N.
 DR Pfam; PF00134; cyclin_1.
 DR Pfam; PF02984; cyclin_C; 1.
 DR SMART; SM00385; CYCLIN_2.
 DR PROSITE; PS00232; CYCLIN_1.
 KW Cyclin; Cell cycle; Cell division; Multigene family.
 FT CONFLICT 288 288 C -> G (IN REF. 3).
 SEQUENCE 376 AA; 42747 MW; FBB95B6BC435FAC2 CRC64;

Query Match	Score	DB 1;	Length
Best Local Similarity	35.1%	398;	376;
Matches 106;	Pred. No.	4.e-26;	
Conservative	Nimatches	96;	
10;	Indels	62;	Gaps 11;

Qy 9 SLLCTRSNVDEGMIVDETPI-EIISIPONGFSQS--ESEEEITIMMVEKEKQHLESDDY 63
 Db 21 ALYCEEKWDDEGEVTEENSSLSSSSPFVVLQQDIFWEDDLVTIFSKEEQGUSCLD- 79

Qy 64 IKRLRSGGDLDLNWKGRDAIWNWKACEVHQGPICFLCLAMNYLDRLPSVHDLPSCKGWII 123
 Db 80 -----DVYLSTDREAVGWLRYNAHYGFSTIAAVLAITYLDKTCISYSLQRDPWMIL 132

Qy 124 QLVAYCISLAAKVEETEVPMILIDIQGDDOFVPEAKSFORMELLYLNKUKWRLRAITPC 183
 Db 133 QLVSYAISLAAKVEETQVPLLDQVEETKVKVFRAKTIQMELLILSTLEWKMLITPI 192

Qy 184 SYTRFLR-----MSKCDQEPNSNTLISRSLQVIASSTTKGIDLEFRPSEAAA 232
 Db 193 SFVDHIRRGLKNNAHWDPLNKH-----RLLSVISDSRFTGYLPSTMVAA 240

Qy 233 VALVSYGELQRVHFDNSFF-SPLFLSQ--KERVKKIGEMIBSDGSIDLCSQTPNGYLEVS 289
 Db 241 TMMRTEQVD--PFDPDLSYQTNLQLVNLTKEKVKTCD-----YDLIQLP-----VD 285

Qy 290 ACCFP-----KTHDSSSS 303
 Db 286 RICLQIQIQQSSKKRKSHDSSSS 307

RESULT 4

CGDI_XENIA	STANDARD;	PRT;	291 AA.
ID CGDI_XENIA			
AC P50755;			
DT 01-OCT-1996 (Rel. 34, Created)			
DT 01-OCT-1996 (Rel. 34, Last sequence update)			
DT 16-OCT-2001 (Rel. 40, Last annotation)			
DB G1/S-specific cyclin D1.			
GN CCND1.			
Xenopus laevis (African clawed frog).			
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;			
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;			
Xenopodidae; Xenopus.			
NCBI_TaxID:8355;			
[1]			
RN SEQUENCE FROM N.A.			
RA Cockrell M.J.; Hunt T.;			
RL Submitted (JUL-1995) to the EMBL/GenBank/DBJ databases.			
-- FUNCTION: Essential for the control of the cell cycle at the G1/S transition.			

RT embryogenesis".
 RL Biophys. Acta 1264:257-260(1995).
 CC FUNCTION: Essential for the control of the cell cycle at the G1/S
 (Istart) transition.
 CC -!- SUBUNIT: Interacts with the CDK4 and CDK6 protein kinases to form
 a serine/threonine kinase holoenzyme complex. The cyclin subunit
 imparts substrate specificity to the complex.
 CC -!- SIMILARITY: Belongs to the cyclin family. Cyclin D subfamily.
 CC
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 or send an email to licences@isb-sib.ch).
 CC
 DR EMBL; X87581; CA60885.1; -.
 DR PIR; S62730; S62730.
 DR ZFIN; ZDB-GENE:980526-176; ccndl1.
 DR InterPro; IPR006670; Cyclin.
 DR InterPro; IPR003367; Cyclin_Cterm.
 DR InterPro; IPR005671; Cyclin_N.
 DR Pfam; PF00134; cyclin_1.
 DR Pfam; PF02984; cyclin_C_1.
 DR SMART; SM001385; CYCLIN_1.
 DR PROSITE; PS00092; CYCLINS_1.
 KW Cyclin Cell cycle; Cell division.
 SEQUENCE 291 AA; 33067 MW; FA5274GB1B46D5EF CRC64;
 Query Match 16.0%; Score 253; DB 1; Length 291;
 Best Local Similarity 29.8%; Pred. No. 5.2e-14;
 Matches 76; Conservative 50; Mismatches 101; Indels 28; Gaps 10
 Qy 43 SEEITMEMYEKEKOHLPSSDDYIKRRLSGDIDLNYGRDAINWIWVACZEVHOFGPLCPLA 102
 Db 24 NDRLVLTQTMKAEEENYLPSNYPFKCIVQEIK1PDM- RKIVATWMLIEVCEEQQEEVPLA 81
 Qy 103 MNVLDRFLSVHDLPSGKGWTLQLLAVALSLLAAKTEETEVPMILLDQVGDQFVFEAKSV 162
 Db 82 MNVLDRFLSVEPKTTR -- LQLLCATCHPLASKWTR -- TAEKUCIYTDNSV 132
 Qy 163 Q----RMEFLVINKWKERLRAITPECSYKFLRNSKCDQEPSNTLISRSLOVIASTTK 217
 Db 133 RPEGLQMEALLANLKWDLAVSHTDFIEFLALU-PIHQSKQQLRKHTQFVALCAT 191
 Qy 218 GIDFLERPSEAAAVALSVEGELORVHDNSFSPLFLSLQKERYVKK-IGEMIESGSD 276
 Db 192 DVNFIAASPPSMIAAG---SVAAGVOLYIKSTD---SCLSQSQTNTFLSQVIRSPD 243
 Qy 277 L--CSOTPGSYLEVS 289
 Db 244 LRSQCBQIEBSLLESS 258

CC -!- FUNCTION: Essential for the control of the cell cycle at the G1/S
 CC (start) transition. Interacts with the CDK4 and CDK6 protein
 CC kinases (By similarity). Belongs to the cyclin family. Cyclin D subfamily.

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CC	RA	Hosokawa Y., Onga T., Nakashima K.: Induction of D2 and D3 cyclin-encoding genes during promotion of the G1/S transition by prolactin in rat Nb2 cells.,";
CC	RT	"Induction of D2 and D3 cyclin-encoding genes during promotion of the G1/S transition by prolactin in rat Nb2 cells.,";
CC	RL	Gene 147:249-252 (1994).
CC	CC	-!- FUNCTION: Essential for the control of the cell cycle at the G1/S (start) transition.
CC	CC	-!- SUBUNIT: Interacts with the CDK4 and CDK6 protein kinases to form a serine/threonine kinase holoenzyme complex. The cyclin subunit imparts substrate specificity to the complex.
CC	CC	-!- SIMILARITY: Belongs to the cyclin family. Cyclin D subfamily.
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CC	CC	DR EMBL; L09752; AAA41010.1; -.
CC	DR	DR EMBL; D16308; EAA03815.1; -.
CC	DR	DR PIR; I58372; I58372.
CC	DR	DR PIR; JC4011; JC4011.
CC	DR	DR InterPro; IPR006670; Cyclin.
CC	DR	DR InterPro; IPR006670; Cyclin_Cterm.
CC	DR	DR Pfam; PF00134; cyclin_1.
CC	DR	DR Pfam; PF02984; cyclin_C_1.
CC	DR	DR SMART; SM00385; CYCLIN_1.
CC	DR	DR PROSITE; PS00232; CYCLINS_1.
CC	DR	Cyclin; Cell cycle; Cell division; Multigene family; Proto-oncogene.
CC	FT	FT CONFFLICT 68 E -> V (IN REF. 2).
CC	FT	FT CONFFLICT 104 C -> V (IN REF. 2).
CC	FT	FT CONFFLICT 232 T -> A (IN REF. 2).
CC	SEQUENCE	SEQUENCE 288 AA; 32826 MN; 4B522BF4E9835FC1 CRC64;
Qy	Query Match Score 15.3%; Best Local Similarity 28.8%; Matches 82; Sequence 29 AA; Score 244.5%; Pred. No. 2.7e-13; Best Local Similarity 28.8%; Pred. No. 2.7e-13; Score 244.5%; Pred. No. 2.7e-13; Length 292; Mismatches 49; Indels 55; Gaps 12;	
Db	YQ	YQ 43 SBEIMMVEKEKQHPLSDYIKRRLGDLINVGRDALLWIKRACEVFGPLCFLA 102
Db	YQ	YQ 24 NDRVLQTMKLAETCTPSVSYFKVCQKEILPQM-RKIVATWMLCEQKCEEEVPLA 81
Db	YQ	YQ 103 MNYLDRFLSHDPLPSGKWLQOLLAVALSIAAKIEETEVPMFLIDLOVGDPOFVFAKSV 162
Db	YQ	YQ 82 MNYLDRFLSFPLKKSR--LQLLGATCMFYASKMKT-IPI---TAEKUCIYDDNSI 132
Db	YQ	YQ 163 Q----RMEILYLNKLKWRRLATITPCSYIYRTRKMSKCDQEPNTLISRSIQL-VASTT 216
Db	YQ	YQ 133 RPEDELLMELLIVNKLKWNLAAMTPHPDFIEHLTOMPLA-BDTKQIURHAQTFLVALC 190
Db	YQ	YQ 217 KGIDLEFPRPSAAAVALSVSGLQRFHFDNS---SFSPFLSLOK-----BVKKI 266
Db	YQ	YQ 191 TDVKFLSNPSPNTAACG---SIVAAVGQIHLGNTNTFLSYCQUTHLSQVTKCDPDCLRAC 247
Db	YQ	YQ 267 GEMIES-----DGSDLCSQTPNQGYLEVS 289
Db	YQ	YQ 248 QEQISSLLESSLURQAQQHNVSETKTVDEADL-SCTPTDVRDVN 291
RESLT	7	YQ VACLSAAKIBETEVFMLIDLVQGDQFVFEAKSVORMELL----VLNKLKWRLRAITP 182
CGD2_RAT	STANDARD;	DB 102 AVCMFAISKIKET-1FL-----TAKRLCYTIDNSYKPOQUELWNLVGLKLNLAAYTP 155
AC	Q04827;	Qy 183 CSYIRYPLRKMSKCDQEPNTLISRSIQL-VASTTQIDPLEFRSS-AAAAVALSVSGE 240
DT	01-OCT-1993	DT 156 HDFIEELRLRKPQ-QKEKLSLIRKAOTFIALCATDFKAMYPPSMATGSVGAICGL 213
DT	01-OCT-1993	DT 241 LQRVHFHDNSSFSPFLSLOKERVKVKGIGEMIESGDSLCSQTPNQGYLEVSACCFSFKTHDS 300
DT	16-OCT-2001	DT 214 QDDEENNALICDALTLLTKHTHDV-----DCLKACQEIQEAVLNLNSLQQFRQBOHQNG 267
DE	G1/S-specific cyclin D2 (Vin-1 proto-oncogene).	DE 301 SSS 303
OS	Rattus norvegicus (Rat).	DB 268 SKS 270
OC	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;	
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.	
OX	NCBI_TaxID=10116;	
RN	[1]	
RP	SEQUENCE FROM N.A. MEDLINE=93275661; PubMed=8502486;	RESULT 8
RA	Hanna Z., Jankowski M., Tremblay P., Jiang X.M., Milatovich A.,	CGD2_MOUSE
RA	Francie U., Jolicœur P.	ID CGD2_MOUSE STANDARD; PRT; 289 AA.
RT	"The Vin-1 gene, identified by provirus insertional mutagenesis, is the cyclin D2."	DT 01-APR-1993 (Rel. 25, Created)
RT	Oncogene 8:1661-1666 (1993).	DT 01-APR-1993 (Rel. 25, Last sequence update)
RN	[2]	DT 16-OCT-2001 (Rel. 40, Last annotation update)
RP	SEQUENCE FROM N.A. MEDLINE=95011623; PubMed=7926809;	DE G1/S-specific cyclin D2.
RX		

DR	GO; GO:0016538; F: cyclin-dependent protein kinase, intrinsic . . . ; IDA.		
DR	GO; GO:000320; P: entry into mitotic cell cycle; IDA.		
DR	InterPro; IPR006670; Cyclin.		
DR	InterPro; IPR004367; Cyclin_Cterm.		
DR	InterPro; IPR006571; Cyclin_N.		
DR	Pfam; PF0134; cyclin_1.		
DR	SMART; SM00385; CYCLIN_2.		
DR	PROSITE; PS00592; CYCLINS_1.		
KW	Cyclin; Cell cycle; Cell division; Multigene family.		
SQ	SEQUENCE 295 AA; 33428 MW; 3A79736B4163251B CRC64;		
Query Match	15.1%; Score 239; DB 1; Length 295;	RN	
Best Local Similarity	28.5%; Pred. No. 7.9e-1; Gaps 12;	RX	SEQUENCE FROM N.A.
Matches	83; Conservative 50; Mismatches 11B; Indels 40; Gaps 12;	RA	Rieder M.J., Livingston R.J., Daniels M.R., Montoya M.A., Chung M.-W.,
Qy	6 LELSLCCTESNVDEGMIYDTEPILEISIPIOMGFSQSESEIIIMMVEKEKQHLPSSDDYIK 65	RA	Miyamoto K.E., Nguyen C.P., Nguyen D.A., Poel C.L., Robertson P.D.,
Db	1 MEHQLLCCCV-----ET-IRRAYPTDNLL--NDVRLRAMLKTETTCAPSVSFK 46	RL	Schackwitz W.S., Sherwood J.K., Wittek L.A., Nickerson D.A.; Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases.
Qy	66 RLRSQDLDLINVGRDALLNIWKACEVHQFQPLCFLANNYLDREFLSVHDJPSGKGWILQL 125	RX	SEQUENCE FROM N.A.
Db	47 CVQKBIVPSM--RKIVATNMLEVCEEQKQEEVPLANNYLDRELSLBPFLKSR--IQL 101	RA	TISSUE=brain, and Placenta;
Qy	126 LAYATCSLIAKIEETEVPMILDLQVGDPRQFEAKRSVQ---RMELAVLNKLKWLRAI 180	RA	RA MEDLINE=223386257; PubMed=12477932;
Db	102 LGATCMFVASSKMKET-IPL---TAEKULCIYTNSIRPELLOMELLINVKWNLLAM 155	RA	RA Klausner R.D., Feingold R.L., Strasbourg G.J., Peigne L.H., Grouse L.H., Schuler G.D.,
Qy	181 TPCSYTRYFLRKMSKCDQPFNSNTLJSRSLQVIASSTKQDFLEFRPSEAAAYALSVSGE 240	RA	RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Db	156 TPHDIEHFVSKMPEAD-ENQQTIRKHAOTFVALCATDVFIFISNPSPMVAAG--SYVAA 211	RA	RA Hopkins R.F., Jordan H., Moore T., Max S.J., Wang J., Hsieh F.,
Qy	241 LQRVTFDNSSSPSPLFSLQQKERVVKIGEMTESSDL--CSQTPNGVLEVS 289	RA	RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Db	212 MQGMLNLG---SPNNFLSCRTTHFLSRVTKCDPDCLRAQEQTAEALLSES 258	RA	RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RESULT 10		RA	RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J., Borak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villaion D.K., Muzy N.D.M., Sodergren E.J., Lu X., Gibbs R.A.,
CG31_HUMAN	ID CG31_HUMAN STANDARD; PRT; 295 AA.	RA	RA Fahey J., Helton E., Ketteman M., Madan A., Rodriguez S., Sanchez A., Blakesley R.W., Touchman J.W., Green B.D., Bouffard G.G., Rodriguez A.C., Grimwood J., Schmitz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smilis D.E.,
AC	P24385;	RA	RA Schnier A., Schein J.B., Jones S.J.M., Marrs M.A./
DT	01-MAR-1992 (Rel. 21, Created)	RA	RA "Generation and initial analysis of more than 15,000 full-length
DT	01-MAR-1992 (Rel. 42, Last sequence update)	RT	RT human and mouse cDNA sequences";
DT	10-OCT-2003 (Rel. 42, Last annotation update)	RL	RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
DE	GN CCND1 OR PRAD1 OR BCL1.	RX	RX INTERACTION WITH CDK4 AND CDK6.
OS	Homo sapiens (Human).	RA	RA MEDLINE=9414440; PubMed=830265;
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	RA	RA Bates S., Bonetta L., McAlain D., Parry D., Holder A., Dickson C., Peters G.;
CC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	RA	RA "CDK6 (PLSTIRE) and CDK4 (PSK-J3) are a distinct subset of the cyclin-dependent kinase complex. The cyclin subunit
NCBI_TaxID	NCBI_TaxID=9606;	CC	CC interacts with the CDK4 and CDK6 protein kinases to form a serine/threonine kinase holoenzyme complex. The cyclin subunit
OX	[1]	CC	CC imparts substrate specificity to the complex.
RN	RN	CC	CC -1 - DISEASE: Involved in B-cell lymphocytic malignancy (particularly mantle-cell lymphoma (MCL)) by a chromosomal translocation t(11;14) (Q13-Q32) that involves CCND1 and immunoglobulin gene
RP	SEQUENCE FROM N.A.	CC	CC (start) translocation. Activation of CCND1 may be oncogenic by
RX	MEDLINE=91194766; PubMed=1826542;	CC	CC directly altering progression through the cell cycle.
RA	Motokura T., Bloom T., Kim H.G., Jueppner H., Rudeerman J.V.,	CC	CC -1 - SUBUNIT: Interacts with the CDK4 and CDK6 protein kinases to form a serine/threonine kinase holoenzyme complex. The cyclin subunit
RA	Kronenberg H.M., Arnold A.,	CC	CC -1 - CCNC1 (PLSTIRE) and CCND1 (PSK-J3) are a distinct subset of the cyclin-dependent kinase complex that associate with cyclin D1.;
RA	"A novel cyclin encoded by a bcl1-linked candidate oncogene.";	CC	CC -1 - Oncogene 9:71-79 (1994).
RT	Nature 350:512-515(1991).	CC	CC -1 - FUNCTION: Essential for the control of the cell cycle at the G1/S (start) transition.
RN	RN	CC	CC -1 - CCNC1 (PLSTIRE) and CCND1 (PSK-J3) are a distinct subset of the cyclin-dependent kinase complex that associate with cyclin D1.;
RP	SEQUENCE FROM N.A.	CC	CC -1 - CCNC1 (PLSTIRE) and CCND1 (PSK-J3) are a distinct subset of the cyclin-dependent kinase complex that associate with cyclin D1.;
RX	MEDLINE=92005671; PubMed=1833066;	CC	CC -1 - CCNC1 (PLSTIRE) and CCND1 (PSK-J3) are a distinct subset of the cyclin-dependent kinase complex that associate with cyclin D1.;
RA	Lew D.J., Dulic V., Reed S.J.,	CC	CC -1 - CCNC1 (PLSTIRE) and CCND1 (PSK-J3) are a distinct subset of the cyclin-dependent kinase complex that associate with cyclin D1.;
RT	"Isolation of three novel human cyclins by rescue of G1 cyclin (Cln) function in yeast.";	CC	CC -1 - CCNC1 (PLSTIRE) and CCND1 (PSK-J3) are a distinct subset of the cyclin-dependent kinase complex that associate with cyclin D1.;
RN	Cell 66:1197-1206(1991).	CC	CC -1 - SIMILARITY: Belongs to the cyclin family. Cyclin D subfamily.
RP	SEQUENCE FROM N.A.	CC	CC -1 - DATABASE: NAME=Atlas Genet. Cytogenet. Oncol. Haematol.; WWW="http://www.infobioigen.fr/services/chromcancer/genes/BCL1.html".
RX	Xiong Y., Connolly T., Futcher B., Beach D.;	CC	CC This SWISS-PROT entry is copyright. It is produced through a collaboration
RT	"Human D-type cyclin."	CC	CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
RL	Cell 65:691-699(1991).	CC	CC the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
RN	[4]	CC	CC use.
RP	SEQUENCE FROM N.A.	CC	CC

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SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RX MEDLINE:93310551; PubMed:8336937;
RA Tamura K.; Kaneko Y.; Jinno S.; Nagata A.; Ogiso Y.; Shimizu K.,
RA Hayakawa T.; Nojima H.; Okayama H.;
RT "Cyclin G: a new mammalian cyclin with homology to fission yeast
C1g1.";
RT [2];
RL Oncogene 8:2113-2118(1993).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE:95011382; PubMed:7980531;
RA Bianchi S.; Fabiani S.; Muratori M.; Arnold A.; Sakaguchi K.; Miki T.,
RA Brandi M.L.;
RT "Calcium modulates the cyclin D1 expression in a rat parathyroid cell
line";
RL Biochem Biophys Res Commun 204:691-700(1994).
CC -!- FUNCTION: Essential for the control of the cell cycle at the G1/S
CC -!- (start) transition. Interacts with the CDK4 and CDK6 protein
CC kinases.
CC -!- SIMILARITY: Belongs to the cyclin family. Cyclin D subfamily.
CC ---
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CC ---
CC EMBL; D14014; BAA03115..1; -.
CC DR EMBL; X75207; CAA53020..1; -.
CC DR PIR; JC2342; JC2342.
CC DR InterPro; IPR006670; Cyclin_Cterm.
CC DR InterPro; IPR003367; Cyclin_Cterm.
CC DR InterPro; IPR006671; Cyclin_N.
CC DR PAM; PF00134; cyclin_1..
CC SMART; SM00385; CYCLIN_1..
CC PROSITE; PS00292; CYCLINS_1..
CC PROSITE; PS00292; CYCLIN; 1..
CC Cyclin; Cell cycle; Cell division; Multigene family; Proto-oncogene;
Chromosome translocation.
CONFLICT 130 N -> G (IN REF. 3).
CONFLICT 168 169 MP -> IA (IN REF. 2).
CONFLICT 188 188 L -> S (IN REF. 3).
SEQUENCE 295 AA; 33729 MW; CRC64;

Query Match 14.9%; Score 236; DB 1; Length 295;
Best Local Similarity 28.7%; Mismatches 51; Indels 44; Gaps 13;
Matches 84; Conservative 51;

6 LELSLCTESNVDEGMIVDDETPIEIISIPIQMGPQSSEBEIMEMVEKEQHLPSDDYIK 65
1 MEHQOLLCCV-----ET-IRRAYDANLII--NDRVRLAMLKAEETCAPSVSYFK 46

66 RLRSGLDLDINVGRDALNIIWKAECBVRQGFLCPCLAMNYLDRLFSLVHDLPSGKGWTIQL 125
47 CVQKEVLPSM-RKIVATMMLVEEQKCEEVPFLANYYLDRLFSLVEPKSKR--IQL 101

126 LAYACSLAAKIEETEVPMFLIDLQVGDPEVFEAKSVO---RMELLVNLKWKRLRAI 180
102 LGATCMFVASKMKT-IPU----TAEKCIYTDNSIRBELLQMLLIVNLKWNLA 155

181 TPCSYIRFLRKMSKCDQEPSNTLISRSIQV-TASITRGIDLEFRPS-EAAAVALSVS 238
156 TPHDIEHFLSKMP--EAENKQTLRKHPQTVALCATVKELSNPPSMVAGSVVIAVQ 213

239 GELORVHFNNSSSPFLSILQKEPVKKIGEMISGDSI--CSQTPNPEVLEVS 289
214 GLNLR-----SPNNFESYYRLTRFLSRVICKDPDCRACQEQUIALELESS 258

QY 6 LEISLCTESNVDEGMIVDDETPIEIISIPIQMGPQSSEBEIMEMVEKEQHLPSDDYIK 65
1 MEHQOLLCCV-----ET-IRRAYDANLII--NDRVRLAMLKAEETCAPSVSYFK 46

66 RLRSGLDLDINVGRDALNIIWKAECBVRQGFLCPCLAMNYLDRLFSLVHDLPSGKGWTIQL 125
47 CVQKEVLPSM-RKIVATMMLVEEQKCEEVPFLANYYLDRLFSLVEPKSKR--IQL 101

126 LAVACSLAAKIEETEVPMFLIDLQVGDPEVFEAKSVO---RMELLVNLKWKRLRAI 180
102 LGATCMFVASKMKT-IPL---TAEKCIYTDNSIRBELLQMLLIVNLKWNLA 155

QY 181 TPSYIYFLRKMSKCDQEPSNTLISRSIQV-TASITRGIDLEFRPS-EAAAVALSVS 239
DB 156 TPHDIEHFLSKMPADE--NKQIIRKHAQTFVALCATVKELSNPPSMVAG--SVVA 210

QY 240 ELQRVHFNDNSSPFLSILQKEPVKKIGEMISGDSI--CSQTPNPEVLEVS 289
DB 211 AMQGLNG---SPNNFESYYRLTRFLSRVICKDPDCRACQEQUIALELESS 258

CCND1.

Rattus norvegicus (Rat).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
[1]

RESULT 12
CCD2_HUMAN
ID CGD2_HUMAN STANDARD:
AC P30279; Q19575; DT 01-APR-1993 (Rel. 25, Created)
AC P30279; Q19575; DT 01-APR-1993 (Rel. 25, Last sequence update)
AC P30279; Q19575; DT 15-JUL-1999 (Rel. 38, Last annotation update)
AC P30279; Q19575; DT 15-JUL-1999 (Rel. 38, Last annotation update)
AC P30279; Q19575; DT 15-JUL-1999 (Rel. 38, Last annotation update)
AC P30279; Q19575; DT 15-JUL-1999 (Rel. 38, Last annotation update)

DT 01-APR-1993 (Rel. 25, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE GI/S-specific cyclin D2.
 GN CCND2.
 OS Homo sapiens (Human).
 OC Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 RN NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE:92347851; PubMed=1386336;
 RX Xiong Y., Menninger J., Beach D., Ward D.C.;
 RA "Molecular cloning and chromosomal mapping of CCND genes encoding
 RT human D-type cyclins".
 RT human D-type cyclins".
 RL Genomics 13:575-584 (1992).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE:93205384; PubMed=845931;
 RA Palmero I., Holder A., Sinclair A.J., Dickson C., Peters G.;
 RT "Cyclins D1 and D2 are differentially expressed in human B-lymphoid
 cell lines";
 RL Oncogene 8:1049-1054 (1993).
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Miyajima N.; Submitted (MAR-1993) to the EMBL/GenBank/DDBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.
 RX Rieder M.J., Livingston R.J., Braun A.C., Montoya M.A., Chung M.-W.,
 RA Miyamoto K.E., Nguyen C.P., Nguyen D.A., Poel C.L., Robertson P.D.,
 RA Schackwitz W.S., Sherwood J.K., Wittek L.A., Nickerson D.A.;
 RA Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
 RN [5]
 RP SEQUENCE FROM N.A.
 RX TISSUE=bone marrow;
 MEDLINE:22388257; PubMed=12477932;
 RA Strausberg R.L., Beingold E.A., Grouse L.H., Derge J.G., Derge J.G.,
 RA Shemesh C.M., Wagner L., Schuler G.D., Schuler G.D.,
 RA Altschul S.F., Collins F.S., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Matsushita K., Farmer M.P., Rubin G.M., Hong L.,
 RA Stepanov M., Soares M.B., Bonoaldo M.P., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S., Loquai L.A., Peters G.J., Abramson R.D., Mullany S.J.,
 RA Bobak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon J., Muniz D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahay J., Heitton E., Ketteman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Rodriguez R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
 RA Schnarch A., Schein J.B., Jones S.J.M., Marra M.A.,
 RA "Generation and initial analysis of more than 15,000 full-length
 human and mouse cDNA sequences".
 Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [6]
 RP SEQUENCE OF 1-240 FROM N.A.
 RX TISSUE=Placenta;
 MEDLINE:92347850; PubMed=1386335;
 RA Inaba T., Matsushima H., Valentine M., Roussel M.F., Sherr C.J.,
 RA Look A.T.;
 RT "Genomic organization, chromosomal localization, and independent
 expression of human cyclin D genes.";
 RL Genomics 13:565-574 (1992).
 CC !- FUNCTION: Essential for the control of the cell cycle at the G1/S
 CC (start) transition.
 CC |- SUBUNIT: Interacts with the CDK4 and CDK6 protein kinases to form
 CC a serine/threonine kinase holoenzyme complex. The cyclin subunit
 CC imparts substrate specificity to the complex.
 CC |- SIMILARITY: Belongs to the cyclin family. Cyclin-D subfamily.
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 DR EMBL; M90813; AAAS51926.1; -;
 DR EMBL; X68452; CAIA48453.1; -;
 DR EMBL; D13639; BAA02802.1; -;
 DR EMBL; AF518005; AAM51041.1; -;
 DR EMBL; BC10958; AAH1958.1; -;
 DR EMBL; M88033; AAAS51928.1; -;
 DR EMBL; M88080; AAAS51928.1; JOINED.
 DR EMBL; M88081; AAAS51928.1; JOINED.
 DR EMBL; M88082; AAAS51928.1; JOINED.
 DR PIR; A42822; A42822.
 DR Genew; HGNC:1583; CCND2.
 DR GR; P31279; -;
 DR MIM; 123833; -;
 DR InterPro; IPR006670; Cyclin.
 DR InterPro; IPR003467; Cyclin_Cterm.
 DR InterPro; IPR006671; Cyclin_N.
 DR Pfam; PF01324; cyclin_1.
 DR Pfam; PF02984; cyclin_C.
 DR SMART; SM00385; CYCLIN.
 DR PROSITE; PS00092; CYCLINS.
 KW Cyclin; Cell cycle; Cell division; Multigene family.
 FT CONFLICT 166 167 KL > H (IN REF. 6).
 FT CONFLICT 224 224 T > H (IN REF. 6).
 SQ SEQUENCE 289 AA; 33067 MW; E45EEF47DD76D30 CRC64;
 Query Match 14.7%; Score 232; DB 1; Length 289;
 Best Local Similarity 28.0%; Pred. No. 3e-12;
 Matches 89; Conservative 50; Minmatches 111; Indels 68; Gaps 16;

QY 8 LSLLCTEEN---VDDEGMIVDTEPIEISIPOMGFSOSESEBIIIMMEMVEKEQKHLPSDD 62
 DR 1 MELICHEVDPPVRARVNRLD-----DRVLQNLITIBERYLQCS 42
 QY 63 YIKRLRSQDLDLNGGRDADLNWKACEVHQFQPLCFLAMMYLDRFLSVHDLPSGKWI 122
 DR 43 YFKCVQK-DIQPYM-RRMATNMLEVCEEQKBEEVFPLAMMYLDRFLA--GVPTPKSH- 97
 DR 123 LQLIVAVACLSIAAKTIEETEVPMILDQVGDQFVFEEKSVORMEL----VNLKIKWRL 177
 DR 98 LQJGJAVOMFLASKLKETS-PL----TAEKUICITYNSIKQBLLEVELVYLGLKWL 151
 QY 178 RAIATPCSYIRYFLRKMSKCDQEPSNTLJSRSLOV-JASTTKGIDEFLFRPSE-AAAVAL 235
 DR 152 AAVTPHDTEHILRKLPQ--QREKSLSLRKHTQFTIALCATDFKAPPMSMTAGSVA 209
 QY 236 SVSGELQRVHFMDNFSFLPSLQK----ERVKIGEMIES-----DGS 275
 DR 210 AICGQODBEVSSLTCDALTELLAKLTNTDVCLKACQEQLBAVLLNSLQQTYRQDDGGS 269
 QY 276 ---DLCSQ--TPNGVLEY 288
 DR 270 KSEDELDQASPTPDVRDI 287

RESULT 13
 CGD2_CHICK STANDARD; PRT; 291 AA.
 ID CGD2_CHICK
 AC P49706;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 01-OCT-2001 (Rel. 40, Last annotation update)
 DE G1/S-specific cyclin D2.
 GN CCND2.
 OC Gallus gallus (Chicken).
 OC Gallirallus metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;

CCNE1 OR CCNE			
OS Homo sapiens (Human);		"Activation of cyclin E/CDK2 is coupled to site-specific autophosphorylation and ubiquitin-dependent degradation of cyclin E.";	
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.			
NCBI_TaxID=9606;			
[1]			
SEQUENCE OF 8-410 FROM N.A.			
RX MEDLINE=92005673; PubMed=1833068;	RT "Cyclin E2, a novel human G1 cyclin and activating partner of CDK2 and Cdk3, is induced by viral oncogenes.";		
RX MEDLINE=99054678; PubMed=9840943;	RT TISSUE SPECIFICITY.		
RA Zarjwala M., Liu J., Xiong Y.;	RT Oncogene 17:2787-2798(1998).		
RA Koff A., Cross F., Fisher A., Schumacher J., le Guellec R., Philippe M., Roberts J.M.,	CC -!- FUNCTION: Essential for the control of the cell cycle at the G1/S (start) transition.		
RA "Human cyclin E, a new cyclin that interacts with two members of the CDK2 gene family";	CC -!- SUBUNIT: Interacts with a member of the CDK2/CDK protein kinases to form a serine/threonine kinase holoenzyme complex. The cyclin subunit imparts substrate specificity to the complex. Interacts with retinoblastoma binding protein 3 and retinoblastoma-like protein 1.		
RA Cell 66:1217-1228(1991).	CC -!- SUBCELLULAR LOCATION: Nuclear.		
RN SEQUENCE OF 8-410 FROM N.A.	CC -!- ALTERNATIVE PRODUCTS:		
RX MEDLINE=92005671; PubMed=1833066;	CC Event=Alternative splicing; Named isoforms=2;		
RA Lew D.J., Dulic V., Reed S.I.;	CC Name=EW1;		
RA "Isolation of three novel human cyclins by rescue of G1 cyclin (Cln) function in yeast";	CC IsoID=24864-1; Sequence=Displayed;		
RT Cell 66:1197-1206(1991).	CC Name=E1S;		
RN SEQUENCE FROM N.A. (ISOFORM E1L).	CC IsoID=24864-2; Sequence=VSP_001253;		
RA Rieder M.J., Livingston R.J., Braun A.C., Montoya M.A., Chung M.-W., Nguyen D.A., Poel C.L., Robertson P.D.,	CC Note=Lacks 49 residues within the cyclin box and cannot complex with CDK2;		
RA Schackwitz W.S., Sherwood J.K., Witkra L.A., Nickerson D.A.;	CC -!- TISSUE SPECIFICITY: Highly expressed in testis and placenta. Low levels in bronchial epithelial cells.		
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.	CC -!- PTM: PHOSPHORYLATION BY CDK2 TRIGGERS ITS RELEASE FROM CDK2 AND DEGRADATION VIA THE UBIQUITIN PROTEASOME PATHWAY (BY SIMILARITY).		
[4]	CC -!- SIMILARITY: Belongs to the cyclin family. Cyclin E subfamily.		
RP SEQUENCE FROM N.A. (ISOFORM E1L).	CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).		
RC TISSUE=Placenta;	CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).		
RX MEDLINE=22388257; PubMed=12477932;	CC DR EMBL; M73812; -; NOT_ANNOTATED_CDS.		
RA Klausner R.D., Collins F.S., Wagner L., Shemesh C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.P., Blatt N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J.J., Hsiao F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stepleton M., Soares M.B., Bondon M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Uedin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahay S.J., Borak S.A., McEwan P.J., McFernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Munro D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Halton E., Kettman M., Mddan A., Rodriguez S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.C., Blakesley R.W., Touchman J.W., Green F.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers P.M., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalius D.E., Schnarch A., Schein J.E., Jones S.J.M., Marra M.A.;	CC DR EMBL; A518727; AA51403.1; ALT_INIT.		
RA "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences";	CC DR EMBL; BC035498; AAH35498.1; -.		
RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).	CC DR EMBL; X95406; CA464687.1; -.		
RN SEQUENCE OF 1-42 FROM N.A.	CC DR EMBL; X95406; CA464688.1; -.		
RX MEDLINE=86226347; PubMed=8649818;	CC DR EMBL; U40788; AAA83269.1; -.		
RX Geng Y., Eaton E.M., Picon M., Roberts J.M., Lundberg A.S., Gifford A., Sardet C., Weinberg R.A.;	CC DR EMBL; U40787; AAA83269.1; -.		
RA "Regulation of cyclin E transcription by E2Fs and retinoblastoma protein";	CC DR PIR; A40270; A40270.		
RT Oncogene 12:1173-1180(1996).	CC DR Genew; HGNC:1.589; CCNE1.		
RN [7] ALTERNATIVE SPlicing.	CC DR GK; P24864; -.		
RX MEDLINE=94266393; PubMed=8207080;	CC DR MIM:123837; C: nucleus; NAS.		
RA Li H., Lanti J.M., Valentine M., Saito M., Reed S.I., Look T., Kidd V.J.;	CC DR GO; GO:0000082; P:G1/S transition of mitotic cell cycle; NAS.		
RA Submitted (DEC-1995) to the EMBL/GenBank/DBJ databases.	CC DR InterPro; IPR006670; Cyclin.		
RN SEQUENCE OF 281-370 FROM N.A.	CC DR InterPro; IPR004367; Cyclin_Cterm.		
RA Li H., Lanti J.M., Valentine M., Saito M., Reed S.I., Look T., Kidd V.J.;	CC DR InterPro; IPR006671; Cyclin_N.		
RN ALTERNATIVE SPlicing.	CC DR Pfam; PF00134; cyclin_C.		
RX MEDLINE=97015119; PubMed=8861947;	CC DR SMART; SM00385; CYCLIN_1.		
RA "Alternative splicing of human cyclin E";	CC DR PROSITE; PS00292; CYCLINS_1.		
RT "Alternative splicing of human cyclin E";	CC DR KW Cyclin; Cell cycle; Cell division; Alternative splicing; Phosphorylation; Missing (in isoform E1S).		
RL J. Cell Sci. 107:581-588(1994).	CC DR FT VARPLIC 154 196 /FTD=VSP_001253.		
RN Best Local Similarity 26.0%; Pred. No. 2.1e-08;	CC DR FT CONFLICT 281 281 L->M (IN REF. 5).		
RX Matches 71; Conservative 49; Mismatches 102; Indels 51; Gaps 12;	CC DR SEQNCB 410 AA; 47077 MW; 424DF0253B/047E CRC64;		
RN Won K.A., Reed S.I.;	CC DR Query Match 11.9%; Score 188.5; DB 1;		
RX MEDLINE=97015119; PubMed=8861947;	CC DR Best Local Similarity 26.0%; Pred. No. 2.1e-08;		
RA	CC DR Matches 71; Conservative 49; Mismatches 102; Indels 51; Gaps 12;		

```

9 SLLCTESNVDEGMIVDET-PIEISIPQMG----FSQSESEEITIMEMVEKEKQHLPSSD 62
Db 73 SLIPTPDKEEDDRVENSTCKPRITAPSRSPLPVSPLWYKIMNEKTYLDRDH 132
Qy 63 YIKR--LRSGDLINVGRODANMWMKACBYHQSPLCFLANNYLDRFLSVHDLPSKG 120
Db 133 FLEQBHLQPKRM---RAILDDMLMEVCYVKLHRETFYLAQDFDRYMATOB--NYVK 185
Qy 121 WILQLAVACUSLAANKTEEVPMILDQVGDPOQVF----EAKSYORMELLVLNK 174
Db 186 TLLQJGISSSFIAKKEIYPPKL----HQPAYVTGACSSDEILTMEMLMKALK 238
Qy 175 WRLRAITPCSYIRYFLRKMSKCD-----QEPSENTLISRSLSOVIASTKGIDFLEFRPS 227
Db 239 WLSPITIVSYLNVMQVAYINDLHEVLLQYPQOIFI-QIAELLDLCVLDVDCLDEF-BY 296
Qy 228 EAAAVALSYSGELQRVHFNDNSSPSPLFSLQK 260
Db 297 GILAASAL-----YHFSSS-----ELNQK 315

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Search completed: March 23, 2004, 16:38:03
 Job time : 19 secs

GenCore version 5.1.6
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OM protein - protein search, using SW model

Run on: March 23, 2004, 16:34:50 ; Search time 46 Seconds
(without alignments)

2112.600 Million cell updates/sec

Title: US-09-530-209A-2
Perfect score: 1583
Sequence: 1 MAEENIELSLCITESNVDDE.....SACCFSFKTHDSSSSYTHLS 308

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters:

1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_insect:*
- 8: sp_organelle:*
- 9: sp_phage:*
- 10: sp_plant:*
- 11: sp_rabbit:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_bacteriophage:*
- 16: sp_virus:*
- 17: sp_archaea:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB	ID	Description
1	1583	100.0	308	10	Q9XFR7		Q9xfr7 arabidopsis
2	1579	99.7	308	10	Q9KFP7		Q9kfp7 arabidopsis
3	1565	98.9	308	10	QBLGA1		Qbla1 arabidopsis
4	954	60.3	317	10	Q9LX96		Q9lx96 arabidopsis
5	722.5	45.6	354	10	Q9ZRX9		Q9zrx9 nicotiana t
6	660.5	41.7	372	10	P93103		P93103 chenopodium
7	653.5	41.3	382	10	Q8LGU0		Q8lgu0 daucus caro
8	621.5	39.3	358	10	Q8S524		Q8s524 zea mays (m
9	614.5	38.8	356	10	Q8SBC0		Q8sbc0 oryza sativ
10	554.5	35.0	390	10	Q8S522		Q8s522 zea mays (m
11	521.5	32.9	356	10	Q8LHA8		Q8lha8 oryza sativ
12	440.5	27.8	315	10	Q8GV0		Q8gv0 helianthus
13	44.0	27.8	360	10	Q8GS62		Q8gs62 physconitre
14	40.9	25.8	350	10	Q7XAB6		Q7xab6 euhorbia e
15	39.1	24.7	330	10	Q9SNV2		Q9snv2 antirrhinum
16	390.5	24.7	343	10	Q9SNV1		Q9snv1 antirrhinum

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

RESULT 1
Q9XFR7
ID Q9XFR7; PRELIMINARY;
AC Q9XFR7; PRT; 308 AA.
DT 01-NOV-1999 (TREMBLrel. 12, Created)
DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE D-type cyclin.
GN CYCA_1.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophytina; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis;
NCBI_TaxID=37022;
OX [1] —

RN SEQUENCE FROM N.A.
RP de Veylder L., De Almeida Engler J., Burssens S., Manevski A.,
RA Lescure B., Van Montagu M., Engler G., Inze D.;
RT "A new D-type cyclin of Arabidopsis thaliana expressed during lateral
root primordia formation.";
RT Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
RL CC -1 SIMILARITY: BELONGS TO THE CYCLIN FAMILY.
DR EMBL; AJ131636; CAB41347; 1; -
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0009101; P:cytokinesis; IEA.
DR GO; GO:0000074; P:regulation of cell cycle; IEA.
DR InterPro; IPR006670; Cyclin.
DR InterPro; IPR004367; Cyclin_Cterm.
DR InterPro; IPR006671; Cyclin_N.
DR Pfam; PF00134; cyclin; 1.
DR Pfam; PF02984; cyclin_C; 1.
DR SMART; SM00385; CYCLIN; 1.
DR PROSITE; PS00292; CYCLINS; 1.
DR KW Cell cycle; Cell division; Cyclin.
DR SEQUENCE 308 AA; 34687 MW; 591ADA3361DD63D CRC64;

Query Match 100.0%; Score 1583; DB 10; Length 308;
Best Local Similarity 100.0%; Pred. No. 1..3e-139; Mismatches 0; Indels 0; Gaps 0;
Matches 308; Conservative 0;

Qy	1 MAEENLELSSLCTESNYDDEGMIVDETPIEISIPIOMGFSQSESEEITIMEMVEKEKOHLPs Db	Db	61 DDYIKRRLRSGLDLDLNVRGRDALNWIWKADEVHQGPLCCLAMNYLDRFLSVHDLPSKGK 120
Db	61 DDYIKRRLRSGLDLDLNVRGRDALNWIWKADEVHQGPLCCLAMNYLDRFLSVHDLPSKGK 120	Qy	121 WILQOLAVACLSAAKIEETEVPMILDLQVGDQPVFEAKSFORMELLVNLNKLKHRLRAI 180
Qy	61 DDYIKRRLRSGLDLDLNVRGRDALNWIWKADEVHQGPLCCLAMNYLDRFLSVHDLPSKGK 120	Db	121 WILQOLAVACLSAAKIEETEVPMILDLQVGDQPVFEAKSFORMELLVNLNKLKHRLRAI 180
Db	61 DDYIKRRLRSGLDLDLNVRGRDALNWIWKADEVHQGPLCCLAMNYLDRFLSVHDLPSKGK 120	Qy	181 TPCSYTRYFURKMSKCDQEPEBTNTLSSRSLOVIASTKGIDFLEPPESEAAAVALSVSGE 240
Qy	121 WILQOLAVACLSAAKIEETEVPMILDLQVGDQPVFEAKSFORMELLVNLNKLKHRLRAI 180	Db	181 TPCSYTRYFURKMSKCDQEESNTLISRSLOVIASTKGIDFLEPPESEAAAVALSVSGE 240
Db	121 WILQOLAVACLSAAKIEETEVPMILDLQVGDQPVFEAKSFORMELLVNLNKLKHRLRAI 180	Qy	241 LQRVHFNDNSSPFLPLFLLQERVKRGIGEMTESGSDPLCSQTPTNGVLEVSACFCFSKTHDS 300
Qy	181 TPCSYTRYFURKMSKCDQEPEBTNTLSSRSLOVIASTKGIDFLEPPESEAAAVALSVSGE 240	Db	241 LQRVHFNDNSSPFLPLFLLQERVKRGIGEMTESGSDPLCSQTPTNGVLEVSACFCFSKTHDS 300
Db	181 TPCSYTRYFURKMSKCDQEPEBTNTLSSRSLOVIASTKGIDFLEPPESEAAAVALSVSGE 240	Qy	301 SSSYTHLS 308
Qy	241 LQRVHFNDNSSPFLPLFLLQERVKRGIGEMTESGSDPLCSQTPTNGVLEVSACFCFSKTHDS 300	Db	301 SSSYTHLS 308
Db	241 LQRVHFNDNSSPFLPLFLLQERVKRGIGEMTESGSDPLCSQTPTNGVLEVSACFCFSKTHDS 300	RESULT 3	
Qy	301 SSSYTHLS 308	Q8LGAI	PRELIMINARY;
Db	301 SSSYTHLS 308	ID Q8LGAI	PRT; 308 AA.
RESULT 2		AC Q8LGAI;	
Q9FKP7		DT 01-OCT-2002 (TREMBLrel. 22, Created)	
Q9FKP7		OS Arabidopsis thaliana (Mouse-ear cress).	
Q9FKP7		OS Arabidopsis; Viridiplantae; Streptophytina; Embryophyta; Tracheophyta;	
Q9FKP7		OC Eukaryota; Magnoliophyta; Magnoliopsida; eudicotyledons; core eudicots; rosids;	
Q9FKP7		OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.	
Q9FKP7		NCBI_TAXID:3702;	
Q9FKP7		RN [1]	
Q9FKP7		SEQUENCE FROM N.A.	
Q9FKP7		RP Brover V., Troukhan M., Alexandrov N., Lu Y.-P., Flavell R.,	
Q9FKP7		RP Feldmann K.; Haas B.J., Volkovska N., Town C.D., Troukhan M., Alexandrov N.,	
Q9FKP7		RP Feldmann K.A., Flavell R.B., White O., Salzberg S.L.;	
Q9FKP7		RP "Full-length messenger RNA sequences greatly improve genome annotation"; RT Genome Biol. 0:0-0(2002).	
Q9FKP7		RN [2]	
Q9FKP7		RP SEQUENCE FROM N.A.	
Q9FKP7		RA Brover V., Troukhan M., Alexandrov N., Lu Y.-P., Flavell R.,	
Q9FKP7		RA Feldmann K.; Haas B.J., Volkovska N., Town C.D., Troukhan M., Alexandrov N.,	
Q9FKP7		RA Feldmann K.; RT "Full-length mRNA from Arabidopsis thaliana.",	
Q9FKP7		RA "Full-length cDNA from Arabidopsis thaliana.",	
Q9FKP7		RA Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.	
Q9FKP7		RT -I SIMILARITY: BELONGS TO THE CYCLIN FAMILY.	
Q9FKP7		RT EMBL: AY084386; AMM60963; 1; -	
Q9FKP7		RT GO: 0005534; C:nucleus; IEA.	
Q9FKP7		RT DR GO: 0000910; P:cyclokinin; IEA.	
Q9FKP7		RT DR GO: GO-0000074; P:regulation of cell cycle; IEA.	
Q9FKP7		RT DR InterPro; IPR006670; Cyclin.	
Q9FKP7		RT DR InterPro; IPR003367; Cyclin_Cterm.	
Q9FKP7		RT DR InterPro; IPR006671; Cyclin_N.	
Q9FKP7		DR DR Pfam; PF00134; cyclin.	
Q9FKP7		DR DR SMART; SM00385; cyclin_C.	
Q9FKP7		DR DR PROSITE; PS00092; CYCLINS; 1.	
Q9FKP7		KW Cell cycle; Cell division; Cyclin.	
Q9FKP7		SEQUENCE 308 AA; 3478B MN; EB077DA1868DC42 CRC64;	
Q9FKP7		Query Match 98.9%; Score 1565; DB 10; Length 308;	
Q9FKP7		Best Local Similarity 99.0%; Pred. No. 6..3e-138; Indels 0; Gaps 0;	
Q9FKP7		Matches 305; Conservative 1; Mismatches 2; Indels 0; Gaps 0;	
Q9FKP7		Qy	1 MARENELSLCLCTESNYDDEGMIVDETPIEISIPIOMGFSQSESEEITIMEMVEKEKOHLPs 60
Q9FKP7		Db	1 MARENELSLCLCTESNYDDEGMIVDETPIEISIPIOMGFSQSESEEITIMEMVEKEKOHLPs 60
Q9FKP7		Qy	1 MARENELSLCLCTESNYDDEGMIVDETPIEISIPIOMGFSQSESEEITIMEMVEKEKOHLPs 60
Q9FKP7		Db	1 MARENELSLCLCTESNYDDEGMIVDETPIEISIPIOMGFSQSESEEITIMEMVEKEKOHLPs 60
Q9FKP7		Qy	1 DDYIKRRLRSGLDLDLNVRGRDALNWIWKADEVHQGPLCCLAMNYLDRFLSVHDLPSKGK 120
Q9FKP7		Db	1 DDYIKRRLRSGLDLDLNVRGRDALNWIWKADEVHQGPLCCLAMNYLDRFLSVHDLPSKGK 120

Qy	121 WIQLAVACIISLAAKIEETEVPMILIDLOQDPQFVFEAKSVORMELLYVNLKIKWRLRAI 180	Db	175 SYVRYFPLSKINGYDQEPPHSRLVTRSLQVIASTTKGDRGLFFFKGVLIVDVWAGIDFLRF 234
Db	121 WIQLAVACIISLAAKIEETEVPMILIDLOQDPQFVFEAKSVORMELLYVNLKIKWRLRAI 180	Qy	225 RPSEAAATVALSYGELQRYHFDNSFSPLFSLQKERYTKIGMIESGDSLCSQTPTNG 284
Qy	181 TPCSYTRYFLRKMSKCDQEPNTLTSRSLQVIASTTKGDFLEFRPSEAAYAVALSVSGB 240	Db	235 RASEAAATVALSYGEE--HFDEPSFSFSQSSSSQTPTNN 290
Db	181 TPCSYTRYFLRKMSKCDQEPNTLTSRSLQVIASTTKGDFLEFRPSEAAYAVALSVSGB 240	Qy	285 -VLEVSACCF- -SKTHDSSSSYTHLS 308
Qy	241 LQRVHFDNSFSPLSLQKERYTKIGMELSDSDICSGCPTPNGLEYVSACCFSPKTHDS 300	Db	291 TVLQFKSRRYSHSLSTASYSSLTSLSL 317
Db	241 LQRVHFDNSFSPLSLQKERYTKIGMELSDGDLSFTPTNGLEYVSACCFSPKTHDS 300	RESULT 5	
Qy	301 SSSYTHLS 308	Q9ZRX9	PRELIMINARY;
Db	301 SSSYTHLS 308	ID	PRT; 354 AA.
RESULT 4			
AC	Q9JX96 PRELIMINARY;	AC	Q9ZRX9;
DT	01-OCT-2000 (TREMBrel. 15, Created)	DT	01-MAY-1999 (TREMBrel. 10, Last sequence update)
DT	01-JUN-2003 (TREMBrel. 15, Last annotation update)	DT	01-JUN-2003 (TREMBrel. 10, Last annotation update)
DE	Cyclin D2.1 protein	DE	Cyclin D2.1 protein
GN	CYCD2.1.	GN	CYCD2.1.
OS	Nicotiana tabacum (Common tobacco)	OS	Nicotiana tabacum (Common tobacco)
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicots; asterids; lamiids; Solanales; Solanaceae; Nicotiana.	OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicots; asterids; lamiids; Solanales; Solanaceae; Nicotiana.
RN	[1]	RN	[1]
RP	SEQUENCE FROM N.A.	RP	SEQUENCE FROM N.A.
RA	Bevan M., Bancroft I., Mewes H.W., Rudd S., Lemcke K., Mayer K.F.X.; Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.	RA	Bevan M., Bancroft I., Mewes H.W., Rudd S., Lemcke K., Mayer K.F.X.; Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.
RN	[2]	RN	[2]
RP	SEQUENCE FROM N.A.	RP	SEQUENCE FROM N.A.
RA	EU Arabidopsis sequencing project; Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.	RA	EU Arabidopsis sequencing project; Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.
CC	-1- SIMILARITY: BELONGS TO THE CYCLIN FAMILY.	CC	-1- SIMILARITY: BELONGS TO THE CYCLIN FAMILY.
DR	AL39395; CAB89199.1; --.	DR	AL39395; CAB89199.1; --.
PIR	T49995; T49995.	PIR	T49995; T49995.
GO	GO:000534: C:nucleus; IEA.	GO	GO:000534: C:nucleus; IEA.
DR	GO; GO:000074: P:cyclokinesis; IEA.	DR	GO; GO:000074: P:cyclokinesis; IEA.
DR	GO; GO:000074: P:regulation of cell cycle; IEA.	DR	GO; GO:000074: P:regulation of cell cycle; IEA.
DR	InterPro; IPR006670; Cyclin.	DR	InterPro; IPR006670; Cyclin.
DR	InterPro; IPR004367; Cyclin_Cterm.	DR	InterPro; IPR004367; Cyclin_Cterm.
DR	PFAM; PF00134; cyclin_1.	DR	PFAM; PF00134; cyclin_1.
DR	SMART; SM00385; CYCLIN_1.	DR	SMART; SM00385; CYCLIN_1.
DR	PROSITE; PS00292; CYCLINS_1.	DR	PROSITE; PS00292; CYCLINS_1.
KW	Cell cycle; Cell division; Cyclin.	KW	Cell cycle; Cell division; Cyclin.
SQ	SEQUENCE 354 AA; 39714 MW; 18363A0E786E89BF CRC64;	SQ	SEQUENCE 354 AA; 39714 MW; 18363A0E786E89BF CRC64;
Query Match			
Best Local Similarity 45.6%; Length 354;			
Matches 164; Conservative 60; Mismatches 76; Indels 41; Gaps 10;			
Qy	1 MAENL---ELSLLCIETESNV---DDEGMIVDETPEBISIPQMGSFQ-----S 41	Qy	1 MAENL---ELSLLCIETESNV---DDEGMIVDETPEBISIPQMGSFQ-----S 41
Db	1 MAADNIXDFEVASNLCLCTKSLCFDDYDLTSLSIQNTEKTSKDSPNNGIRSEPLIDLP 60	Db	1 MAADNIXDFEVASNLCLCTKSLCFDDYDLTSLSIQNTEKTSKDSPNNGIRSEPLIDLP 60
Query Match			
Best Local Similarity 45.6%; Length 354;			
Matches 164; Conservative 60; Mismatches 76; Indels 41; Gaps 10;			
Qy	2 ESEETIEMVEKEKOHLPSSDYKIKLRSGLDLNLYGRDAALWINKACEVHQFGPLFCFL 101	Qy	2 ESEETIEMVEKEKOHLPSSDYKIKLRSGLDLNLYGRDAALWINKACEVHQFGPLFCFL 101
Db	61 LSBECLSFMRVEMEFPKDQDYYVERLRSQGDLDSV RKEALDWIKAHMNYGFGELSFCL 119	Db	61 LSBECLSFMRVEMEFPKDQDYYVERLRSQGDLDSV RKEALDWIKAHMNYGFGELSFCL 119
Query Match			
Best Local Similarity 60.3%; Length 317;			
Matches 212; Conservative 23; Mismatches 58; Indels 34; Gaps 8;			
Qy	3 ENLELSLCTESNVDEGMIWDETPLEISIPTONGFSOSESERIMENVEKEKOHLPSSDDY 63	Qy	102 AMNYLDPLSYHDLPSGGKWLQLLAVACIISLAAKTEETEPMLDLQVGDPQFYFEAKS 161
Db	3 EMPEPNLV--SNFDEDKNSVDTR--SIFQMGF-PLESBIVREMIEKRQHSPRDY 55	Db	120 SINYLDPLSYHDLPSKTWVQLLAVACIISLAAKTEETEPMLDLQVGDPQFYFEAKS 179
Qy	64 QIILAVACIISLAAKIEETEVPMILIDLOQDPQFVFEAKSVORMELLYVNLKIKWRLRAITPC 123	Qy	162 VORMELLYVNLKIKWRLRAITPCSYTRFLRMSKCDQEPTNTLISLSQVTAStTKGIDF 221
Db	56 LKRLRGDLDENV-RIQALGWIKWACBFLQPLCIAAMMYLDRFLSYHDLPSGGKWL 114	Db	180 IQRMELLVLSLTKWQMAQPYTFDYMFKMANG-DQIPRPLISGMQJLSSIRSIDP 238
Qy	124 QIILAVACIISLAAKIEETEVPMILIDLOQDPQFVFEAKSVORMELLYVNLKIKWRLRAITPC 183	Qy	222 LEFRPSEAAAVALSYGELORVHEDNNSFSPLFSL-LQKERVKIGEME----- 271
Db	115 QIILAVACIISLAAKIEETEVPMILIDLOQDPQFVFEAKSVORMELLYVNLKIKWRLRAITPC 174	Db	239 LEFRSSEIAASVAMSYSGEQAKDIDKA -MPCFFTHLDKGRVQCVELIQDLTTATIT 296
Qy	184 SYTRYFLRKMSKCDQEPNTLTSRSLQVTAStTK-----GIDFLF 224	Qy	272 SDGSDLCSQTPTNGVLEVSACCFSFKTHD-----SSSSYT 305

DR	SMART; SM00385; CYCLIN; 1.	Matches 119; Conservative 49; Mismatches 89; Indexes 11; Gaps 6;
DR	PROSITE; PS0292; CYCLINS; 1.	
KW	Cell cycle; Cell division; Cyclin.	
SEQUENCE	390 AA; 42016 MW; 1CE006BE20DABF70 CRC64;	
Query Match	Score 554.5%; DB 10; Length 390;	
Best Local Similarity	35.01%; Pred. No. 2, 8e-43;	
Matches 135; Conservative 52; Mismatches 89; Indels 9;		
Db	10 LILCETSNVQD---DEGMIVDTPEIESTPQMGSQS-----ESEETIMERVEK 53	QY
Db	13 LLCAEBEHSSILWYDB----BEEEEEAVGRRGRGPQSEECVAGLVER 68	Db
QY	54 EKHLPSDDOYIKRLRSGGIDLNVRDALKWNLINKACEVHQFGPLCFLAMNYLDRELSVH 113	Db
Db	69 ERDIMPGPXGYDRLRGCCGLCVK-RREADWINKAYTHFRPLTAYLVNLYDREFLSLS 127	QY
QY	114 DLPGKGKWMLQQLLAVACSLAAKTBETEPMLDLQVGQPQFVFEAKSVORMELLVNLK 173	Db
Db	128 EVPDGKDQDNNTQQLLAVACSLAAKMEVAPQCLDLQVGEARYFEAKTVORMELLVTL 187	QY
QY	174 KWRLRAITTCSTYFLRMSK-CDQEPEANTLISRSLQVIASTTKGIDLEFRPSEAAA 232	Db
Db	188 NWRMHATFESFYDYLFLNKLSNGOSTAPSCWLLQSAELILRARGTGCVGFRPSEAAA 247	RESULT 12
QY	233 VALVSGLQQR-----VHFDFNSSFSPFLSLQERVKKGEMTESDGSPLC----- 278	OBGV0
Db	248 VAAVAGDDADGVENACAHVD-----KERVLRQEAIGMSAAGDGA 295	ID Q8GV0
QY	279 -----SQTPNGLVLEVSACCFSFKTHDSSS 303	PRELIMINARY;
Db	296 TVPBKSARRSSPVPPVPPQSPVGVLDAAACLSVSEEEATA 339	PRT; 315 AA.
QBLHA8	OBGV0; PRELIMINARY;	
AC	PRT; 356 AA.	
QBLHA8; ID	OBGV0; PRELIMINARY;	
DT	01-OCT-2002 (TREMBLrel. 22, Created)	
DT	01-OCT-2002 (TREMBLrel. 22, Last sequence update)	
DE	0594D10.18 protein.	
GN	0594D10.18.	
OS	Oryza sativa (japonica cultivar-group).	
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;	
OC	Spermatophyta; Magnoliophyta; eudicots; asterids;	
OC	campanulids; Asterales; Asteraceae; Heliantheae,	
NCBI_TaxID	39947; NCBI_TaxID=4233;	
RN	[1] SEQUENCE FROM N.A.	
RP	Freeman D., Murray J.A.H.	
RA	"Isolation, characterization and expression of cyclin and cyclin-dependent kinase genes in Jerusalem Artichoke (Helianthus tuberosus)." ;	
RT	Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.	
RT	DR EMBL; AY063460; AAL4/479.-;	
RT	DR GO; GO:0005634; C:nucleus; IEA.	
RT	DR InterPro; IPR006670; Cyclin.	
RT	DR InterPro; IPR004367; Cyclin_Cterm.	
RT	DR InterPro; IPR006571; Cyclin_N.	
DR	PFam; PF00134; cyclin_1.	
DR	PFam; PF02984; cyclin_C; 1.	
DR	SMART; SM00385; CYCLIN; 1.	
DR	PROSITE; PS000292; CYCLINS; 1.	
SQ	SEQUENCE FROM N.A.	SEQUENCE 315 AA; 35651 MW; 8P35A49F1097C308 CRC64;
RC	Strain=cv. Nipponbare;	
RA	Sasaki T., Matsumoto T., Yamamoto K.;	
RT	"Oryza sativa nipoobare (GA3) genomic DNA, chromosome 7, PAC clone: P0594D10.";	
RT	Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.	
CC	-!- SIMILARITY: BELONGS TO THE CYCLIN FAMILY.	
DR	Gramene; Q8IRAB; -.	
DR	GO; GO:0005634; C:nucleus; IEA.	
DR	GO; GO:000910; P:cytokinesis; IEA.	
DR	GO; GO:000074; P:regulation of cell cycle; IEA.	
DR	InterPro; IPR006670; Cyclin_Cterm.	
DR	InterPro; IPR04367; Cyclin_Cterm.	
DR	InterPro; IPR006671; Cyclin_N.	
DR	Pfam; PF00134; cyclin_1.	
DR	Pfam; PF02984; cyclin_C; 1.	
DR	SMART; SM00385; CYCLIN; 1.	
DR	PROSITE; PS000292; CYCLINS; 1.	
KW	SEQUENCE 356 AA; 39176 MW; 8B8A8BBDDA7A9EEE CRC64;	
SQ	Query Match 32.9%; Score 521.5%; DB 10; Length 356;	
Best Local Similarity	44.4%; Pred. No. 3e-40;	

QY	189	FLRKMSKICQEPSNT----LISRSLQVIASSTTKGIDFLFRPSEAAAVALSVSGELORV	244	GYLEV-----SACCFSPKTHDSSSYT	305	
Db	184	FSHII----DPSAMYTGGLISRQIINNIQEASLLWPSFIIAATILCAASDIF	238	Db	303 GVLDAADVSSPCTVLGFSRESSPDT	330
QY	245	HFDNSSFSLPF-SLIQKERVKIGKEMIEEDGSDLCSQTNGV--LEYSACCFSFKTHDS	300			
Db	239	SLINADHAAESWCDGLSKERIKTCYRLV-----QSPLPVHVRMTARYSTESGDS	289			
QY	301	SSS 303			RESULT 14	
Db	290	SSS 292			Q7XAB6	PRELIMINARY;
					ID Q7XAB6	PRT;
					AC Q7XAB6;	350 AA.
					DT 01-OCT-2003 (TREMBLrel.	25; Created)
					DT 01-OCT-2003 (TREMBLrel.	25; Last sequence update)
					DT 01-OCT-2003 (TREMBLrel.	25; Last annotation update)
					DE Cyclin_D3-1.	
					GN CYCD3-1.	
					OS Euphorbia esula (leafy spurge).	
					OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;	
					OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;	
					OC euroids I; Malpighiales; Euphorbiaceae; Euphorbioideae; Euphorbiae;	
					OC NCBI_TaxID=3193; [1]	
					RN	SEQUENCE FROM N.A.
					RA Horvath D.P.;	
					RT "Cloning of cyclin D3 genes from Euphorbia esula."	
					RL Submitted (JUL-2003) to the EMBL/GenBank/DDBJ databases.	
					DR EMBL; AY340589; AAQ19973.1; -.	
					KW	
					SEQUENCE 350 AA; 39835 MW; CF080F5E07C6C4B5 CRC64;	
					Query Match 25.8%; Score 409; DB 10; Length 350;	
					Best Local Similarity 34.1%; Pred. No. 9.7e-30;	
					Matches 115; Conservative 59; Mismatches 91; Indels 72; Gaps 13;	
					QY 9 SILCTESNVDDEGMIVD-----ETPIEISIPONGFSQSESEEEITMEM 50	
					Db 12 ALYCSEBD-NWEGEVDDIFHEQEDQGENTSVPQNSPVDIN-----WEDEITSVF 62	
					QY 51 VEKEKOHLPSPDYIKURSGDIDN---VGRRDALNWIWAKACEVTFQGFLCFCCLAMNYL 106	
					Db 63 SKQEQQNL---YKK-----LEINPCLAKSRRDADTWMMKVNHYSFALTTSVLFVNFL 112	
					QY 107 DRFLSYHDILPSGKGWMQLQAVACKAEEETEPMLIDLOQGPQFVEAKSVSQRME 166	
					Db 113 DRFLFSDLDLCEKEPKWMTOLTAVALSIAAKVETOPPLLDLQVQVSKYVEAKTQFME 172	
					QY 167 LLVLFNLKWRRAITPSYTRFLRNSKCDQ---EPSNTLJSRSLQVIASTTKGIDFLIE 223	
					Db 173 LLVLSTLQWKRNPVTLSFIDYMTRLGFDYLCWEE---PIRRCELIVLISISDRFIP 228	
					QY 224 FRPSEAAAAYALSVSGEGLORYHFDSFSPLSLL---QKERVKKIGEMI-----270	
					Db 229 YLPSEASA1MHWVINGIEPLGDEFB-TQFGILQDKERVNNCREMITELGSRYYGNQ 287	
					QY 271 ---ESGSDLCSQTPTNGVLEYSSACCPFSKTHDSSSY 304	
					Db 288 SNKRYGSDF-PGSPICMDY---SESSDNNSDW 317	
					RESULT 15	
					Q9SNV2	PRELIMINARY;
					ID Q9SNV2	PRT;
					AC Q9SNV2;	330 AA.
					DT 01-MAY-2000 (TREMBLrel.	13; Created)
					DT 01-MAY-2000 (TREMBLrel.	13; Last sequence update)
					DE Cyclin D1.	
					GN CYCD.	
					OS Antirrhinum majus (Garden snapdragon).	
					OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;	
					OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;	
					OC Lamiales; Plantaginaceae; Antirrhineae; Antirrhinum.	
					OX NCBI_TaxID=4151; [1]	
					RN	

SEQUENCE FROM N.A.
 Gaudin V., Lunness P., Robert P., Towers M., Riou-Khamlich C.,
 Murray J., Coen E., Doonan J.H.;
 RT "The expression of D-cyclin genes define distinct developmental zones
 in Antirrhinum apical meristems and is locally regulated by the
 cyclodella gene.",
 Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
 CC -!- SIMILARITY: BELONGS TO THE CYCLIN FAMILY.
 DR EMBL; A250336; CAB61221.1;
 DR GO; GO:0005634; C:nucleus; IEA.
 DR GO; GO:0000910; P:cytokinesis; IEA.
 DR GO; GO:000074; P:regulation of cell cycle; IEA.
 InterPro; IPR006670; Cyclin.
 InterPro; IPR004367; Cyclin_Cterm.
 DR InterPro; IPR006671; Cyclin_N.
 PFAM; PF00134; cyclin_1.
 PFAM; PF02984; cyclin_C; 1.
 SMART; SM00345; CYCLIN; 1.
 PROSITE; PS00292; CYCLINS; 1.
 KW Cell cycle; Cell division; Cyclin.
 SQ SEQUENCE 330 AA; 3694 MW; 707E9C6382BBED2 CRCC4;
 Query Match 24.7%; Score 391; DB 10; Length 330;
 Best Local Similarity 35.9%; Pred. No. 4.3e-28;
 Matches 104; Conservative 49; Mismatches 9; Indels 46; Gaps 9;
 QY 10 LIICPE-SNV-----DDEGMVNDTPIETISIPQMGPSQSRSRSEELIMENVKERKQHLDSD 62
 Db 12 LLCGEDDSNTIFSGGGDD--LPETTSDSVSIP-----TDVDESIAIGLEDEEDD---- 56
 Qy 63 YIRRLRGSGDLNNG---F RDALANWIKACEVHQFGPLFCCLANNYLDFLSTYHDLSPGK 119
 Db 57 -LAGVNSSSSNQSDSSTSSTESTAWIWKVQRYIGFGPTAYLAVSYFREFLNHHLPKLN 115
 Qy 120 GWIQLLAVALACSLAAKIBETEVMLIDIQVGDPQFVPEAKSVORMELLIYLNKLKWRLRA 179
 Db 116 GWPOLLSSAACSLAAKMEESLVPSLLDQVEGANFIFPRNTORMELIVLRVLDWRLS 175
 Qy 180 ITPGCSYIRFLRKMSKCDQEPNST---LJSRSQVIASSTTKGDELFRPSEAAAAYA 235
 Db 176 ISPPRYLSSPAALKI-----DPTGTYTGFTTSRAKEITLSTQETSLLYRPSCIAATML 230
 Qy 236 SVSGELQRVHFNDNSSFSPFLQKERVVKIGEMIESDSDLCSQTPNCY 285
 Db 231 SSANDL-----PRESFITAQHAIAWCQDGHHKDNTASCTKLIQCY 269

Search completed: March 23, 2004, 16:39:03
 Job time : 49 secs

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PR	18-MAY-1999;	99US-0134768P.	PR	27-JUL-1999;	99US-0145919P.
PR	19-MAY-1999;	99US-0134941P.	PR	28-JUL-1999;	99US-0145951P.
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PR	28-MAY-1999;	99US-0136782P.	PR	04-AUG-1999;	99US-0147302P.
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PR	22-JUN-1999;	99US-0139899P.	PR	16-SEP-1999;	99US-0154138P.
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PR	23-JUL-1999;	99US-0145145P.	PR	22-OCT-1999;	99US-0160981P.
PR	23-JUL-1999;	99US-014518P.	PR	22-OCT-1999;	99US-0160989P.
PR	23-JUL-1999;	99US-014524P.	PR	25-OCT-1999;	99US-0161404P.
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PR	26-OCT-1999;	99US-0161359P.	PR	11-MAY-1999;	99US-0134255P.
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PR	Best Local Similarity 100.0%;	Pred. No. 9-208;	PR	20-MAY-1999;	99US-0135144P.
Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			PR	21-MAY-1999;	99US-0135333P.
Qy	1 MAENNLISLCTESNVDEGMYDEPEIIEISIPQMGPQSSEETIMVEKEKOHLP S 60		PR	24-MAY-1999;	99US-0135623P.
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Qy	61 DDYIKRLRS GDDLNVRGRDAINWIKA CEVHQGPLCFCCLAMNYLDRFLSYHDLPSKG 120		PR	27-MAY-1999;	99US-0136322P.
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Qy	121 WIQLLAVACISLAAKI BETTEVPMILIDLVQGIPQFYFEAKSVORMELLVINKLKWLRLA 180		PR	01-JUN-1999;	99US-0137222P.
Db	121 WIQLLAVACISLAAKI BETTEVPMILIDLVQGIPQFYFEAKSVORMELLVINKLKWLRLA 180		PR	03-JUN-1999;	99US-0137228P.
Qy	181 TPCSYTRYFLRMSKCDQEPENTLISRSIQLQVIASTTKGIDFILEFRSE 228		PR	04-JUN-1999;	99US-0137502P.
Db	181 TPCSYTRYFLRMSKCDQEPENTLISRSIQLQVIASTTKGIDFILEFRSE 228		PR	07-JUN-1999;	99US-0137724P.
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Qy	181 TPCSYTRYFLRMSKCDQEPENTLISRSIQLQVIASTTKGIDFILEFRSE 228		PR	10-JUN-1999;	99US-0138477P.
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Qy	181 TPCSYTRYFLRMSKCDQEPENTLISRSIQLQVIASTTKGIDFILEFRSE 228		PR	16-JUN-1999;	99US-0139522P.
Db	181 TPCSYTRYFLRMSKCDQEPENTLISRSIQLQVIASTTKGIDFILEFRSE 228		PR	16-JUN-1999;	99US-0139533P.
Qy	181 TPCSYTRYFLRMSKCDQEPENTLISRSIQLQVIASTTKGIDFILEFRSE 228		PR	17-JUN-1999;	99US-0139622P.
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Qy	181 TPCSYTRYFLRMSKCDQEPENTLISRSIQLQVIASTTKGIDFILEFRSE 228		PR	12-JUL-1999;	99US-0142970P.
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Qy	181 TPCSYTRYFLRMSKCDQEPENTLISRSIQLQVIASTTKGIDFILEFRSE 228		PR	14-JUL-1999;	99US-0143624P.
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Db	181 TPCSYTRYFLRMSKCDQEPENTLISRSIQLQVIASTTKGIDFILEFRSE 228		PR	21-JUL-1999;	99US-0144484P.
Qy	181 TPCSYTRYFLRMSKCDQEPENTLISRSIQLQVIASTTKGIDFILEFRSE 228		PR	21-JUL-1999;	99US-0144844P.
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Qy	181 TPCSYTRYFLRMSKCDQEPENTLISRSIQLQVIASTTKGIDFILEFRSE 228		PR	21-JUL-1999;	99US-0145088P.
Db	181 TPCSYTRYFLRMSKCDQEPENTLISRSIQLQVIASTTKGIDFILEFRSE 228		PR	22-JUL-1999;	99US-0145055P.
Qy	181 TPCSYTRYFLRMSKCDQEPENTLISRSIQLQVIASTTKGIDFILEFRSE 228		PR	22-JUL-1999;	99US-0145070P.
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EPI03405-A2.

XX

DT 18-OCT-2000 (first entry)

XX

DE Arabidopsis thaliana protein fragment SEQ ID NO: 59334.

XX

KW Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.

XX

OS Arabidopsis thaliana.

XX

PN EPI03405-A2.

XX

PD 06-SEP-2000.

XX

PF 25-FEB-2000; 20000BP-00301439.

XX

PR 25-FEB-1999; 99US-0121825P.

PR 09-MAR-1999; 99US-0123180P.

PR 23-MAR-1999; 99US-0123548P.

PR 16-APR-1999; 99US-0126788P.

PR 19-APR-1999; 99US-0126264P.

PR 29-MAR-1999; 99US-0126785P.

PR 01-APR-1999; 99US-0124462P.

PR 09-APR-1999; 99US-0128234P.

PR 16-APR-1999; 99US-0128714P.

PR 30-APR-1999; 99US-0130077P.

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PR 05-MAY-1999; 99US-0132484P.

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PR	03-AUG-1999;	99US-0147038P.	PR	29-OCT-1999;	99US-0161933P.
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PR	06-AUG-1999;	99US-0147303P.	Matches 207; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
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PR	09-AUG-1999;	99US-0147493P.			
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PR	11-AUG-1999;	99US-0148319P.			
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PR	13-AUG-1999;	99US-0148565P.	Db 1 MIVDETPIEISIPQMGSQSSEETIMMVEKEKQHLPSSDYYIKRRLSGDIDLNVYGRDA 60		
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PR	16-AUG-1999;	99US-0149368P.	Db 61 IINWIWAKACEVHOFGLPCCLANNYLDRFLSYTHDLPSCGKWLQLIAYACLSAAKETE 120		
PR	17-AUG-1999;	99US-0149175P.	Qy 142 VPLMLIDLQVGDQFVFEAKSFORMELIVLNKLWKWRRAITPCSYIYFLRKNSKCQEPS 201		
PR	18-AUG-1999;	99US-0149426P.	Db 121 VPLMLIDLQVGDQFVFEAKSFORMELIVLNKLWKWRRAITPCSYIYFLRKNSKCQEPS 180		
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PR	23-AUG-1999;	99US-0149930P.	Db 181 NTLLISRLSQVIASSTTKGIDLEFLFRSE		
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PR	31-AUG-1999;	99US-0151438P.	XX AC AAY14071;		
PR	01-SEP-1999;	99US-0151930P.	XX DT 16-JUL-1999 (first entry)		
PR	07-SEP-1999;	99US-0152363P.	XX DE Mitogenic cyclin CYCD4 protein sequence.		
PR	10-SEP-1999;	99US-0153070P.	XX KW Mitogenic cyclin; CYCD4; modulator; plant cell cycle; growth inhibitor; plant cell division; cell growth; regulator; cell proliferation; growth regulator; herbicide; cell division progression.		
PR	13-SEP-1999;	99US-0153358P.	XX KW Arabidopsis thaliana.		
PR	15-SEP-1999;	99US-0154018P.	OS XX WO9922002-A1.		
PR	16-SEP-1999;	99US-0154039P.	PN		
PR	20-SEP-1999;	99US-0154779P.	XX		
PR	22-SEP-1999;	99US-0155139P.	PD 06-MAY-1999.		
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PR	29-SEP-1999;	99US-0156596P.	XX PA (CROP-) CRODESIGN NV.		
PR	04-OCT-1999;	99US-0157117P.	XX PI Inze D, De Veylder L, De Almeida J;		
PR	05-OCT-1999;	99US-015753P.	XX DR WPI; 1999-312966/26.		
PR	06-OCT-1999;	99US-0157865P.	XX N-PSDB; AAX36897.		
PR	07-OCT-1999;	99US-0158029P.	XX PT DNA sequence encoding a mitogenic cyclin.		
PR	08-OCT-1999;	99US-0158232P.	XX PS Claim 1; Page 47-49; 57pp; English.		
PR	14-OCT-1999;	99US-0158330P.	XX PR 21-OCT-1999;		
PR	14-OCT-1999;	99US-0158331P.	XX 99US-0160768P.		
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PR	14-OCT-1999;	99US-0159294P.	XX 99US-0160814P.		
PR	18-OCT-1999;	99US-0159538P.	XX 99US-0160815P.		
PR	21-OCT-1999;	99US-0160741P.			
PR	21-OCT-1999;	99US-0160767P.			
PR	21-OCT-1999;	99US-0161920P.			
PR	21-OCT-1999;	99US-0161922P.			
PR	21-OCT-1999;	99US-0161933P.			

CC plant cell division and/or growth, for influencing the activity of
 CC mitogenic cyclin in a plant cell, as positive or negative regulator of
 CC cell proliferation, for modifying the growth inhibition caused by
 CC environmental stress conditions, or for use in a screening method for the
 CC identification of inhibitors or activators of cell cycle proteins. A
 CC compound which is an activator or inhibitor of the mitogenic cyclin can
 CC be used as a growth regulator and/or herbicide. The proteins can also be
 CC used to influence cell division progression in yeast, mammals and insects
 XX

SQ Sequence 308 AA;

Query Match 67.2%; Score 207; DB 2; Length 308;

Best Local Similarity 99.7%; Pred. No. 7.8e-188; Mismatches 0; Indels 0;

Matches 307; Conservative 0; Mismatches 1; Indels 0;

Qy	1	MAEENLSSLCTESNVDDGMINVDEPTEIISIPQMGFSQSSEEEITIMENVEKEQHLPs	60	PR 21-APR-1999; PR 23-APR-1999; PR 23-APR-1999;
Db	1	MAEENLSSLCTESNVDDGMINVDEPTEIISIPQMGFSQSSEEEITIMENVEKEQHLPs	60	PR 28-APR-1999; PR 30-APR-1999; PR 30-APR-1999;
Qy	61	DDYIKRLRSQGDDLNVRGRDAILNWKACRYHQFGLCFLCFCLAMNTLDRELSVHDLPSGKG	120	PR 04-MAY-1999; PR 05-MAY-1999; PR 06-MAY-1999; PR 06-MAY-1999;
Db	61	DDYIKRLRSQGDDLNVRGRDAILNWKACRYHQFGLCFLCFCLAMNTLDRELSVHDLPSGKG	120	PR 07-MAY-1999; PR 11-MAY-1999; PR 14-MAY-1999;
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Qy	181	TPCSYIYRFKMSKCDQEBSNTLISRSLQVIATSTKGIIFLEFRPSEAAAVAVLSVSGE	240	PR 21-MAY-1999; PR 21-MAY-1999; PR 25-MAY-1999;
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Qy	301	SSSYTHLS 308	308	PR 04-JUN-1999; PR 04-JUN-1999;
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RESULT 4

AAG47105 ID AAG47105 standard; protein; 273 AA.

XX Protein identification; signal transduction pathway; metabolic pathway;
 KW hybridisation assay; genetic mapping; gene expression control; promoter;
 KW termination sequence.
 XX Arabidopsis thaliana.
 OS EPI033405-A2.
 XX 06-SEP-2000 (first entry)
 XX 25-FEB-2000; 2000EPB-00301439.

XX	PR 25-FEB-1999;	990US-0121825P	PR 02-JUL-1999; PR 06-JUL-1999;
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PR 19-JUL-1999;	99US-0144325P.		

Query Match 55.5%; Score 171; DB 3; Length 308;
 Best Local Similarity 100.0%; Pred. No. 1.2e-153;
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 Db 1 MAEENIELSLLCTESNDDEGMIVDTPETSI PONGFSQSSEETIMENVEKEHQHLPS 60

Qy 61 DDYIKRLRSGDLDLNGRDLNWIKACETHQFGILCFCLAMNNYLDRFLSVHDLPSKG 120
 Db 61 DDYIKRLRSGDLDLNGRDLNWIKACETHQFGILCFCLAMNNYLDRFLSVHDLPSKG 120

Qy 121 WIQLLAVACSLAAKTEEVPMILDQVGDQPQFVPEAKSVORMELLYIN 171
 Db 121 WIQLLAVACSLAAKTEEVPMILDQVGDQPQFVPEAKSVORMELLYIN 171

RESULT 6
 AAG23338
 ID AAG23338 standard; protein; 287 AA.
 XX DT 17-OCT-2000 (first entry)
 DE Arabidopsis thaliana protein fragment SEQ ID NO: 26609.
 AC AAG23333;
 XX Protein identification; signal transduction pathway; metabolic pathway;
 KW hybridization assay; genetic mapping; gene expression control; promoter;
 KW termination sequence.
 XX Protein identification; signal transduction pathway; metabolic pathway;
 KW hybridization assay; genetic mapping; gene expression control; promoter;
 XX Arabidopsis thaliana.
 XX EP1033405-A2.
 XX PD 06-SEP-2000.
 XX PR 25-FEB-2000; 2000EP-00301439.
 XX PR 05-MAR-1999; 99US-0121825P.
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PR	08-OCT-1999;	99US-0158232P.			

Query Match Score 150; DB 3; Length 287;
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 Db 1 MIVDDEPIEISIPIOMGFSQSESEEITIMEMYEKEKQLHPSDDYIKRIRSGDIDLAVYGRDA 60

Qy 82 LNWIWACVHEQFGPLCFCLAMNYLLDRFLSVDLPGKGWLQLQAVASLAAKETTE 141
 Db 61 LNWIWACVHEQFGPLCFCLAMNYLLDRFLSVDLPGKGWLQLQAVASLAAKETTE 120

Qy 142 VPMLIDLQVGDPQFVPEAKSYORMELVLN 171
 Db 121 VPMLIDLQVGDPQFVPEAKSYORMELVLN 150

RESULT 7

AAG2339

AAG2339 standard; protein; 273 AA.

XX AAG2339;

AC AAG2339;

XX AAG2339;

DT 17-OCT-2000 (first entry)

Arabidopsis thaliana protein fragment SEQ ID NO: 26610. Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.

XX Arabidopsis thaliana.

OS XX EP103405-A2.

XX DT 06-SEP-2000.

XX FF 25-FEB-2000; 2000EP-00301439.

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PR 23-MAR-1999; 99US-0125788P.

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termination sequence.
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PR	07-SEP-1999;	99US-0152363P.			
PR	10-SEP-1999;	99US-0153070P.			
PR	13-SEP-1999;	99US-0153778P.			
PR	15-SEP-1999;	99US-0154018P.			
PR	16-SEP-1999;	99US-0154039P.			
PR	20-SEP-1999;	99US-0154779P.			
PR	22-SEP-1999;	99US-0155139P.			
PR	23-SEP-1999;	99US-0155466P.			
PR	24-SEP-1999;	99US-0155639P.			
PR	28-SEP-1999;	99US-0156488P.			
PR	04-OCT-1999;	99US-0156556P.			
PR	05-OCT-1999;	99US-0157753P.			
PR	06-OCT-1999;	99US-0159244P.			
PR	07-OCT-1999;	99US-0159255P.			
PR	13-OCT-1999;	99US-0159339P.			
PR	14-OCT-1999;	99US-0159310P.			
PR	14-OCT-1999;	99US-0159331P.			
PR	14-OCT-1999;	99US-0159637P.			
PR	14-OCT-1999;	99US-0159638P.			
PR	18-OCT-1999;	99US-0159584P.			
PR	21-OCT-1999;	99US-0160741P.			
PR	21-OCT-1999;	99US-0160767P.			

Query Match Score 13; DB 3; Length 339;
 Best Local Similarity 100.0%; Pred. No. 0.0014;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query 124 QLLAVACLSAAK 136
 ID ABR98363 standard; peptide: 36 AA.
 Db 128 QLLAVACLSAAK 140

RESULT 11
 ID ABR98363
 AC ABR98363;
 DT 17-SEP-2003 (first entry)
 DE Tumour cell growth inhibitor genetic suppressor element peptide SEQ:241.
 KW Human; tumour cell growth inhibiting genetic suppressor element; tumour cell growth inhibitor; breast cancer; tumour; cytostatic; tumour cell growth inhibitor.
 KW Homo sapiens.
 XX WO2003008578-A2.
 XX 30-JAN-2003.
 XX PD 28-FEB-2002; 2002WO-US006254.
 XX PR 20-JUL-2001; 2001US-0306730P.
 XX PA (UNIT) UNIV ILLINOIS FOUND.
 PA Primiano T, Chang B, Roninson IB,
 PA XX WPI; 2003-248013/24.
 PA XX DR
 PA XX PT Identifying compounds that inhibit mammalian genes necessary for tumor cell growth, useful for inhibiting tumor cell growth, by assaying for expression or activity of several genes necessary for tumor cell growth.
 PA XX Claim 22; Page 67: 145pp; English.
 PA XX CC The present invention describes a method (W) for identifying a compound (C) that inhibits growth of a mammalian cell. (M) involves culturing a cell in the presence or absence of (C), assaying the cell for expression or activity of one or more enriched genes (see Table 3 in the specification, G1) that have not been previously implicated in cell proliferation, and identifying (C) when expression or activity of at least one of (G1) is lower in presence of (C) than in absence of (C). Also described in a compound (I) that inhibits tumour cell growth and mammal cell expression or activity of (G1), identified by (M), where (I) is not an inhibitor or RNA synthesis or protein synthesis. (C) and (I) have cytostatic activity and can be used as tumour cell growth.

CC inhibitors. (M) is useful for identifying a compound that inhibits growth
 CC of a mammalian cell preferably a human tumour cell. (I) is useful for
 CC inhibiting tumour cell growth by inhibiting expression of (G1). (I) is
 CC useful for treating a disease or condition relating to abnormal cell
 CC proliferation or tumour cell growth. ACF18360 to ACF1187 and ABR98451 to
 CC ABR98436 represent sequences used in the exemplification of the present
 invention.

SQ Sequence 36 AA;

Query Match 3.6%; Score 11; DB 6; Length 36;

Best Local Similarity 100.0%; Pred. No. 0.014; Indels 0; Gaps 0;

Matches 11; Conservative 0; Mismatches 0;

ACD84709 standard; peptide: 36 AA.

QY 101 LANNYLDRFLS 111

Db 25 LANNYLDRFLS 35

RESULT 12
 ACD84709

ID ACD84709 standard; peptide: 36 AA.

XX AC D84709;

XX DT 01-JAN-2004 (first entry)

XX DE MCF-7 breast cancer cell tumor library GSE peptide #13.

XX KW cytostatic; cell proliferation; tumor; breast cancer cell;

XX genetic suppressor element.

XX OS Homo sapiens.

XX PN WO2003007884-A2.

XX XX PD 31-OCT-2002.

XX KW 14-MAR-2002; 2002WO-EP003768.

XX XX PR 14-MAR-2001; 2001US-0275734P.

XX PN (HYBR-) HYBRIGENICS.

XX XX PI Legrain P, Daviet L;

XX DR WPI; 2003-103412/09.

XX DR N-PSDB; ACA57117.

XX PT New complex between two interacting proteins in adipocyte cells, useful

PT for identifying selected interacting domains that modulate protein

PT interactions, or for preventing or treating metabolic disorders such as

PT obesity or diabetes.

XX XX PS Claim 6; Page 173-174; 382pp; English.

XX XX CC The invention relates to a complex between two interacting proteins in

CC adipocyte cells, given in the specification. The proteins are identified

CC by selecting bait protein from a known adipocyte marker and then

CC performing a yeast 2-hybrid selection to isolate prey proteins encoded by

CC members of an adipocyte cDNA library. The proteins are designated SID

CC (RTM) (selected interacting domains) proteins. Also included are a

CC polynucleotide encoding a polypeptide in the adipocyte cells, a

CC recombinant host cell expressing at least one of the interacting

CC polypeptides of the complex, selecting a modulating compound in adipocyte

CC cells, a SID (RTM) polypeptide comprising any of the 738 amino acid

CC sequences given in the specification (including its fragment or variant),

CC a SID (RTM) polynucleotide comprising any of the 738 nucleotide sequences

CC given in the specification (including its fragment or variant), a vector

CC comprising the SID (RTM) polynucleotide, a recombinant host cell

CC comprising the vector, a protein chip comprising the polypeptides and a

CC record comprising all or part of the data, listed in the specification.

CC The complex, polypeptides, polynucleotides and compounds are useful for

CC preventing or treating metabolic disorders such as obesity or diabetes.

CC The polynucleotides are useful as probes or primers. The complex is

CC particularly useful for identifying selected interacting domains (SID

CC (RTM)) for screening drugs that modulate the protein interaction, thus

CC exhibiting the therapeutic effect. The present sequence represents a SID

CC (prey) protein of the invention.

SQ Sequence 36 AA;

Query Match 3.6%; Score 11; DB 7; Length 36;
 Best Local Similarity 100.0%; Pred. No. 0.014;
 Matches 11; Conservative 0; Mismatches 0; Indels 0;
 Gaps 0;

QY 101 LANNYLDRFLS 111

Db 25 LANNYLDRFLS 35

RESULT 13
 ABU70573

ID ABU70573 standard; protein: 244 AA.

XX AC ABU70573;

XX DT 10-JUN-2003 (first entry)

XX Human adipocyte Selected Interacting domain, SID, #204.

XX DE Human adipocyte SID; selected interacting domain; anorectic;

XX KW anti-diabetic; protein interaction; diabetes;

XX yeast 2-hybrid assay; metabolic disorder; obesity.

XX OS Homo sapiens.

XX PN WO200286122-A2.

XX XX PD 31-OCT-2002.

XX KW 14-MAR-2002; 2002WO-EP003768.

XX XX PR 14-MAR-2001; 2001US-0275734P.

XX PN (HYBR-) HYBRIGENICS.

XX XX PI Legrain P, Daviet L;

XX DR WPI; 2003-103412/09.

XX DR N-PSDB; ACA57117.

XX PT New complex between two interacting proteins in adipocyte cells, useful

PT for identifying selected interacting domains that modulate protein

PT interactions, or for preventing or treating metabolic disorders such as

PT obesity or diabetes.

XX XX PS Claim 6; Page 173-174; 382pp; English.

XX XX CC The invention relates to a complex between two interacting proteins in

CC adipocyte cells, given in the specification. The proteins are identified

CC by selecting bait protein from a known adipocyte marker and then

CC performing a yeast 2-hybrid selection to isolate prey proteins encoded by

CC members of an adipocyte cDNA library. The proteins are designated SID

CC (RTM) (selected interacting domains) proteins. Also included are a

CC polynucleotide encoding a polypeptide in the adipocyte cells, a

CC recombinant host cell expressing at least one of the interacting

CC polypeptides of the complex, selecting a modulating compound in adipocyte

CC cells, a SID (RTM) polypeptide comprising any of the 738 amino acid

CC sequences given in the specification (including its fragment or variant),

CC a SID (RTM) polynucleotide comprising any of the 738 nucleotide sequences

CC given in the specification (including its fragment or variant), a vector

CC comprising the SID (RTM) polynucleotide, a recombinant host cell

CC comprising the vector, a protein chip comprising the polypeptides and a

CC record comprising all or part of the data, listed in the specification.

CC The complex, polypeptides, polynucleotides and compounds are useful for

CC preventing or treating metabolic disorders such as obesity or diabetes.

CC The polynucleotides are useful as probes or primers. The complex is

CC particularly useful for identifying selected interacting domains (SID

CC (RTM)) for screening drugs that modulate the protein interaction, thus

CC exhibiting the therapeutic effect. The present sequence represents a SID

CC (prey) protein of the invention.

SQ Sequence 244 AA;

Query Match 3.6%; Score 11; DB 6; Length 244;
 Best Local Similarity 100.0%; Pred. No. 0.082; Mismatches 0; Indels 0; Gaps 0;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX AAR29310 standard; protein; 295 AA.

Qy 101 LAMNYLDRFLS 111
 ID AAR27114 Standard; protein; 295 AA.
 Db 56 LAMNYLDRFLS 66

AC AAR27114;
 XX DT 25-MAR-2003 (revised)
 XX DT 20-MAY-1998 (first entry)
 DE prad1.
 XX KW Cyclin; embryo; cdc2 protein kinase; parathyroid adenoma; G1;
 XX KW 11q13/11p15; oncogene; cell cycle regulation.
 OS Homo sapiens.
 PN WO9215603-A1.
 XX PD 17-SEP-1992.
 XX PF 11-MAR-1992; 92WO-US001925.
 PR 11-MAR-1991; 91US-00667711.
 PA (GEHO) GEN HOSPITAL CORP.
 XX PI Arnold A;
 XX PS 1; Fig 6; 54pp; English.
 DR WPI; 1992-331664/40.
 DR N-PSDB; AAQ288899.
 XX PT Prad1 cyclin and DNA encoding it - useful in promoting wound healing,
 PT and for diagnosing and treating cancer.
 XX PS Claim 1; Fig 6; 54pp; English.
 DR The sequence given is a novel cyclin, prad1. Cyclins are a class of
 CC eukaryotic proteins which are identified by their cyclic accumulation and
 CC destruction at defined points in embryonic cell cycles. They bind to, and
 CC are essential for activation of, cdc2 protein kinase. The PRAD1 mRNA
 CC sequence was isolated from cells of benign parathyroid adenoma. The
 CC gene was found to map to the 11q13 region and was found to be
 CC overexpressed in those parathyroid adenomas which had a 11q13/11p15
 CC chromosomal rearrangement. The PRAD locus is amplified and expressed in
 CC oncogene which figures in a variety of types of neoplasms. PRAD1 mRNA is
 CC highly conserved across species. PRAD1 mRNA levels fluctuate across the
 CC cell cycle, consistent with, but not proving a role in cell cycle
 CC regulation. The peak in PRAD1 mRNA levels occurs late in the cell cycle
 CC or in G1. (Updated on 25-MAR-2003 to correct PN field.)
 XX SQ Sequence 295 AA;

Query Match 3.6%; Score 11; DB 2; Length 295;
 Best Local Similarity 100.0%; Pred. No. 0.097; Mismatches 0; Indels 0; Gaps 0;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX Qy 101 LAMNYLDRFLS 111
 Db 80 LAMNYLDRFLS 90

XX Search completed: March 23, 2004, 16:46:28
 Job time : 63 secs

RESULT 15

Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 23, 2004, 16:45:23 ; Search time 24 Seconds
 (without alignments)
 662.533 Million cell updates/sec

Title: perfect score:
 Sequence: 308
 Scoring table: OLIGO
 Gapop 60.0 , Gapext 60.0

Searched: 389414 seqs, 51625971 residues

Word size : 0

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
 Maximum DB seq Length: 200000000

Post-processing: Listing first 45 summaries

Database : ISSUED PATENTS AA:*

1: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*

2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*

3: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*

4: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*

5: /cgn2_6/ptodata/2/iaa/5C_PCTUS_COMB.pep:*

6: /cgn2_6/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	13	4.2	335	4 US-09-404-296B-28
2	13	4.2	354	4 US-09-404-296B-2
3	11	3.5	102	US-08-580-988A-23
4	11	3.6	152	2 US-08-460-694-4
5	11	3.6	152	3 US-08-460-744-4
6	11	3.6	152	3 US-08-467-711B-4
7	11	3.6	295	1 US-08-472-893A-8
8	11	3.6	295	1 US-08-472-893A-8
9	11	3.6	295	2 US-08-460-694-2
10	11	3.6	295	2 US-08-464-517-2
11	11	3.6	295	2 US-08-464-517-9
12	11	3.6	295	2 US-08-464-517-9
13	11	3.6	295	2 US-08-246-361A-2
14	11	3.6	295	2 US-08-246-361A-19
15	11	3.6	295	2 US-08-246-361A-20
16	11	3.6	295	3 US-08-463-772-2
17	11	3.6	295	3 US-08-463-772-19
18	11	3.6	295	3 US-08-463-772-20
19	11	3.6	295	3 US-08-460-744-2
20	11	3.6	295	3 US-08-667-711B-2
21	11	3.6	295	3 US-08-947-492-8
22	11	3.6	295	5 PCT-US93-05000-2
23	11	3.6	295	5 PCT-US93-05000-19
24	11	3.6	295	5 PCT-US93-05000-20
25	11	3.6	358	4 US-09-398-858-2
26	11	3.6	358	4 US-09-398-858-2
27	11	3.6	618	2 US-08-770-761A-3

RESULT 1
 US-09-404-296B-28

; Sequence 28, Application US/09404296B
 ; Patent No. 655935A

; GENERAL INFORMATION:

; APPLICANT: MURRAY, James Augustus Henry

; TITLE OF INVENTION: PLANTS WITH MODIFIED GROWTH

; FILE REFERENCE: 2121-0151P

; CURRENT APPLICATION NUMBER: US/09/404,296B

; CURRENT FILING DATE: 1993-09-24

; NUMBER OF SEQ ID NOS: 32

; SOFTWARE: Patentin version 3.1

; SEQ ID NO: 28

; LENGTH: 335

; TYPE: PRT

; ORGANISM: Arabidopsis thaliana

; US-09-404-296B-28

Query Match Similarity 4.2%; Score 13; DB 4; Length 335;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

ALIGNMENTS

QY	124 QLAVACLSIAAK 136
Db	128 QLAVACLSIAAK 140

RESULT 2

; Sequence 2, Application US/09404296B
 ; Patent No. 6559358

; GENERAL INFORMATION:

; APPLICANT: MURRAY, James Augustus Henry

; TITLE OF INVENTION: PLANTS WITH MODIFIED GROWTH

; FILE REFERENCE: 2121-0151P

; CURRENT APPLICATION NUMBER: US/09/404,296B

; CURRENT FILING DATE: 1993-09-24

; NUMBER OF SEQ ID NOS: 32

; SOFTWARE: Patentin version 3.1

; SEQ ID NO: 2

; LENGTH: 354

; TYPE: PRT

; ORGANISM: Nicotiana tabacum

; US-09-404-296B-2

Query Match Similarity 4.2%; Score 13; DB 4; Length 354;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 142 ||||||| QLIQAVACISLAAK 154
 STREET: 1100 New York Avenue, N.W., Suite 600
 CITY: Washington
 STATE: DC
 COUNTRY: USA
 ZIP: 20005

RESULT 3
 US-08-580-988A-23

Patent No. 5,856,611

GENERAL INFORMATION:
 APPLICANT: Aggarwal et al.
 TITLE OF INVENTION: Rumor Necrosis Factor Receptor-I-Associated Protein Kinase And Methods
 TITLE OF INVENTION: For Its Use
 NUMBER OF SEQUENCES: 27

CORRESPONDENCE ADDRESS:
 ADDRESSEE: Dr. Benjamin A. Adler
 STREET: 8011 Candle Lane
 CITY: Houston
 STATE: Texas
 COUNTRY: USA
 ZIP: 77071

COMPUTER READABLE FORM:
 COMPUTER: Floppy disk
 OPERATING SYSTEM: PC-POS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/460,694
 FILING DATE: 02-JUN-1995
 CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
 NAME: McConathy, Evelyn H.
 REGISTRATION NUMBER: 35,279
 REFERENCE/DOCKET NUMBER: 0009.4070002

TELECOMMUNICATION INFORMATION:
 TELEPHONE: 202-371-2600
 TELEX/FAX: 202-371-2540

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 152 amino acids

TYPE: amino acid

STRANDEDNESS: not relevant

TOPOLOGY: linear

MOLECULE TYPE: peptide

Query Match 3.6%; Score 11; DB 2; Length 152;
 Best Local Similarity 100.0%; Pred. No. 0.0095; Mismatches 0; Indels 0; Gaps 0;
 Matches 11; Conservative 0; Missmatches 0;

QY 101 LAMYLDRLFLS 111

Db 25 LAMYLDRLFLS 35

RESULT 5
 US-08-460-744-4

Sequence 4, Application US/08460744

Patent No. 6107541

GENERAL INFORMATION:
 APPLICANT: Arnold, Andrew
 TITLE OF INVENTION: PRADI Cyclin and its cDNA
 NUMBER OF SEQUENCES: 6

CORRESPONDENCE ADDRESS:

ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.

STREET: 1100 New York Avenue, N.W., Suite 600

CITY: Washington

STATE: DC

COUNTRY: USA

ZIP: 20005

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-POS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/460,744

FILING DATE: 02-JUN-1995

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: McConathy, Evelyn H.

REGISTRATION NUMBER: 35,279

REFERENCE/DOCKET NUMBER: 0609.4070005

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-371-2600

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 152 amino acids

RESULT 4

US-08-460-694-4

Sequence 4, Application US/08460694

Patent No. 5,856,655

GENERAL INFORMATION:

APPLICANT: Arnold, Andrew

TITLE OF INVENTION: PRADI Cyclin and its cDNA

NUMBER OF SEQUENCES: 6

CORRESPONDENCE ADDRESS:

ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.

TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: peptide
S-08-460-744-4

; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-460-744-4

; STREET: Steuart Street Tower, 18th Fl., One Market
; STREET: Plaza

Qy	Db	Match	Score	Length	DB	Indels	Gaps
Best Local Similarity	100.0%	Score	11	Length	152		
Matches	11	Pred. No.	0.095				
		Mismatches	0				
101	LAMNYIDRFLS	111					
	DRFLS						
25	LAMNYIDRFLS	35					

CORRESPONDENCE ADDRESS:
ADDRESSEE: Leona L. Lauder
STREET: Stewart Street Tower, 18th Fl., One Market
STREET: Plaza
CITY: San Francisco
STATE: CA
COUNTRY: USA
ZIP: 94105

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

RESULT 6
US-07-667-711B-4
Sequence 4, Application US/0766771B
; Patent No. 6110700
GENERAL INFORMATION:
APPLICANT: ARNOLD, ANDREW
TITLE OF INVENTION: Pradl. Cyclin
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: STEERNE, KESSLER, GOLEN
STREET: 1100 NEW YORK AVE., NW
CITY: WASHINGTON
STATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDTIN: mowr plmowr A-
PLANTIN: mowr plmowr A-

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/947,120
FILING DATE: 19920917
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Lauder, Leona L.
REGISTRATION NUMBER: 30,863
REFERENCE/DOCKET NUMBER: 91-210-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-543-7927
TELEFAX: 415-543-4219
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 295 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-947-120-8

MEDIUM TYPE: FLOPPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: 10607127-31B

Query Match 3.6%; Score 11; DB 1; Length 295;
 Best Local Similarity 100.0%; Pred. No. 0.017%;
 Matches 11; Conservative 0; Mismatches 0; Indels

FILING DATE: 11-MAR-1991
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MCPHAIL, DONALD R.
REGISTRATION NUMBER: 35, 0611
REFERENCE/DOCKET NUMBER: 6019-40700000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 152 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPLOGY: not relevant
MOLECULE TYPE: peptide
US-07-667-71B-4

US-08-472-893A-8
Sequence 8, Application US/08472893A
Patent No. 5,677,130
GENERAL INFORMATION:
APPLICANT: Meeker, Timothy C.
TITLE OF INVENTION: BCL-1 Locus Nucleic Acid Probes and
TIME OF INVENTION: May 1996 Assay Methods
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Leona L. Launder
STREET: Stewart Street Tower, 18th Fl., One Market
CITY: San Francisco, CA 94103

Query Match Similarity 3.6%; Score 11; DB 3; Length 152;
 Best Local Similarity 100.0%; Pred. No. 0; 0.0095;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0

SIRIS: CA
COUNTRY: USA
ZIP: 94105

QY
DB
101 LAMNYLDRFLS 111
111 ||||| |||||
25 LAMNYLDRFLS 35

COMPUTER READABLE FORM
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patient In Reliance #1.0 Version #1 2/20/92

RESULT 7
US-07-947-120-8

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/472,893
FILING DATE: 07 JAN 2008

Patent No. 5538846
GENERAL INFORMATION:
APPLICANT: Meier, Timothy C.
TITLE OF INVENTION: BCL-1 Locus Nucleic Acid Probes and Assay Methods
NUMBER OF INVENTIONS: 10

APPLICATION NUMBER: US 07/947,120
FILING DATE: 17-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Lauder, Leona L.

REFERENCE DOCKET NUMBER: 91-210-1
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 415-777-9257
 TELEFAX: 415-543-4219
 INFORMATION FOR SEQ ID NO: 8:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 295 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-472-893A-8

Query Match 3.6%; Score 11; DB 1; Length 295;
 Best Local Similarity 100.0%; Pred. No. 0.017; 0; Mismatches 0; Indels 0; Gaps 0;

QY 101 LAMNYIDRFLS 111
 Db 80 LAMNYIDRFLS 90

RESULT 9
 US-08-460-694-2

; Sequence 2, Application US/08460694

PATENT NO. 5658655

GENERAL INFORMATION:

APPLICANT: Arnold, Andrew

TITLE OF INVENTION: PRADI Cyclin and its cDNA

NUMBER OF SEQUENCES: 8

CORRESPONDENCE ADDRESS:

ADDRESSEE: STEINE, KESSLER, GOLDSTEIN & FOX P.L.L.C.

STREET: 1100 New York Avenue, N.W., Suite 600

CITY: Washington

STATE: DC

COUNTRY: USA

ZIP: 20005

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PATENT RELEASE #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08460/694

FILING DATE: 02-JUN-1995

CLASSIFICATION: -435

ATTORNEY/AGENT INFORMATION:

NAME: McConathy, Evelyn H.

REGISTRATION NUMBER: 35,279

REFERENCE DOCKET NUMBER: US/08460/694

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-371-2600

TELEFAX: 202-371-2540

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:
 LENGTH: 295 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein

US-08-460-694-2

Query Match 3.6%; Score 11; DB 2; Length 295;
 Best Local Similarity 100.0%; Pred. No. 0.017; 0; Mismatches 0; Indels 0; Gaps 0;

QY 101 LAMNYIDRFLS 111
 Db 80 LAMNYIDRFLS 90

GENERAL INFORMATION:
 APPLICANT: BEACH, David H.
 TITLE OF INVENTION: D-TYPE CYCLIN AND USES RELATED THERETO
 NUMBER OF SEQUENCES: 50
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: LAHIVE & COCKFIELD
 STREET: 60 State Street
 CITY: Boston
 STATE: MA
 COUNTRY: USA
 ZIP: 02109

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: ASCII(text)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/464,517

FILING DATE:

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/963,308

FILING DATE: 16-OCT-1992

APPLICATION NUMBER: US 07/888,178

FILING DATE: 26-MAY-1992

PRIMER APPLICATION DATA:

APPLICATION NUMBER: US 07/701,514

FILING DATE: 16-MAY-1991

ATTORNEY/AGENT INFORMATION:

NAME: Matthew P. Vincent

REGISTRATION NUMBER: 36,709

REFERENCE DOCKET NUMBER: MII-004C

TELECOMMUNICATION INFORMATION:

TELEPHONE: (617) 227-5941

TELEFAX: (617) 227-5941

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 295 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-464-517-2

Query Match 3.6%; Score 11; DB 2; Length 295;
 Best Local Similarity 100.0%; Pred. No. 0.017; 0; Mismatches 0; Indels 0; Gaps 0;

QY 101 LAMNYIDRFLS 111
 Db 80 LAMNYIDRFLS 90

RESULT 11

US-08-460-517-19

; Sequence 19, Application US/08464517

PATENT NO. 569340

GENERAL INFORMATION:

APPLICANT: BEACH, David H.

TITLE OF INVENTION: D-TYPE CYCLIN AND USES RELATED THERETO

NUMBER OF SEQUENCES: 50

CORRESPONDENCE ADDRESS:

ADDRESSEE: LAHIVE & COCKFIELD

STREET: 60 State Street

CITY: Boston

STATE: MA

COUNTRY: USA

ZIP: 02109

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: ASCII(text)

CURRENT APPLICATION DATA:

RESULT 10
 US-08-464-517-2
 ; Sequence 2, Application US/08464517
 ; Patent No. 5869640

APPLICATION NUMBER: US/08/464,517
 FILING DATE: 16-OCT-1992
 CLASSIFICATION: 435
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 07/963,308
 FILING DATE: 26-MAY-1992
 PRIORITY APPLICATION NUMBER: US 07/888,178
 FILING DATE: 16-MAY-1991
 ATTORNEY/AGENT INFORMATION:
 NAME: Matthew P. Vincent
 REGISTRATION NUMBER: 36,709
 REFERENCE/DOCKET NUMBER: MITI-004C
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (617) 227-7400
 TELEX/FAX: (617) 227-5941

SEQUENCE CHARACTERISTICS:
 LENGTH: 295 amino acids
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide

US-08-464-517-19

Query Match 3.6%; Score 11; DB 2; Length 295;
 Best Local Similarity 100.0%; Pred. No. 0.017; Mismatches 0;
 Matches 11; Conservative 0; Indels 0; Gaps 0;

Qy	101 LAMNYLDRFLS 111
Db	80 LAMNYLDRFLS 90

RESULT 12
 US-08-464-517-20
 Sequence 20, Application US/08464517
 Patent No. 589640

GENERAL INFORMATION:
 APPLICANT: BEACH, David H.
 TITLE OF INVENTION: D-TYPE CYCLIN AND USES RELATED THERETO
 NUMBER OF SEQUENCES: 50
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: LAHIVE & COCKFIELD
 STREET: 60 State Street
 CITY: Boston
 STATE: MA
 COUNTRY: USA
 ZIP: 02109

COMPUTER READABLE FORM:
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: ASCII(text)

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/246,361A
 FILING DATE: 19-MAY-1994
 CLASSIFICATION: 435
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 07/963,308
 FILING DATE: 16-OCT-1992
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 07/888,178
 FILING DATE: 26-MAY-1991
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US/08/464,517
 FILING DATE:
 CLASSIFICATION: 435
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/464,517
 FILING DATE:
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 07/963,308
 FILING DATE: 16-OCT-1992
 APPLICATION NUMBER: US 07/888,178
 FILING DATE: 26-MAY-1992
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 07/701,514
 FILING DATE: 16-MAY-1991
 ATTORNEY/AGENT INFORMATION:
 NAME: Matthew P. Vincent
 REGISTRATION NUMBER: 36,709
 REFERENCE/DOCKET NUMBER: MITI-004C
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (617) 227-7400
 TELEX/FAX: (617) 227-5941

SEQUENCE CHARACTERISTICS:
 LENGTH: 295 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein

US-08-464-517-20

Query Match 3.6%; Score 11; DB 2; Length 295;
 Best Local Similarity 100.0%; Pred. No. 0.017; Mismatches 0;
 Matches 11; Conservative 0; Indels 0; Gaps 0;

Qy	101 LAMNYLDRFLS 111
Db	80 LAMNYLDRFLS 90

RESULT 13
 US-08-246-361A-2
 Sequence 2, Application US/08246361A
 Patent No. 5998582

GENERAL INFORMATION:
 APPLICANT: BEACH, David H.
 TITLE OF INVENTION: D-TYPE CYCLIN AND USES RELATED THERETO
 NUMBER OF SEQUENCES: 50
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: LAHIVE & COCKFIELD
 STREET: 60 State Street
 CITY: Boston
 STATE: MA
 COUNTRY: USA
 ZIP: 02109

COMPUTER READABLE FORM:
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: ASCII(text)

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/246,361A
 FILING DATE: 19-MAY-1994
 CLASSIFICATION: 435
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 07/963,308
 FILING DATE: 16-OCT-1992
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 07/888,178
 FILING DATE: 26-MAY-1991
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US/08/464,517
 FILING DATE:
 CLASSIFICATION: 435
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US 07/701,514
 FILING DATE:
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 07/963,308
 FILING DATE: 16-OCT-1992
 APPLICATION NUMBER: US 07/888,178
 FILING DATE: 26-MAY-1992
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 07/701,514
 FILING DATE: 16-MAY-1991
 ATTORNEY/AGENT INFORMATION:
 NAME: Matthew P. Vincent
 REGISTRATION NUMBER: 36,709
 REFERENCE/DOCKET NUMBER: MITI-004C
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (617) 227-7400
 TELEX/FAX: (617) 227-5941

SEQUENCE CHARACTERISTICS:
 LENGTH: 295 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein

US-08-246-361A-2

Query Match 3.6%; Score 11; DB 2; Length 295;
 Best Local Similarity 100.0%; Pred. No. 0.017; Mismatches 0;
 Matches 11; Conservative 0; Indels 0; Gaps 0;

Qy	101 LAMNYLDRFLS 111
Db	80 LAMNYLDRFLS 90

Db 80 |||||LAMNYLDRFLS 90

RESULT 14
 US 08-246-361A-19
 Sequence 19, Application US/08246361A
 Patient No. 599882
 GENERAL INFORMATION:
 APPLICANT: BEACH, David H.
 TITLE OF INVENTION: D-TYPE CYCLIN AND USES RELATED THERETO
 NUMBER OF SEQUENCES: 50
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: LAHIVE & COCKFIELD
 STREET: 60 State Street
 CITY: Boston
 STATE: MA
 COUNTRY: USA
 ZIP: 02109

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: ASCII(text)

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/246,361A
 FILING DATE: 19-MAY-1994
 CLASSIFICATION: 435
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 07/963,308
 FILING DATE: 16-OCT-1992
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 07/888,178
 FILING DATE: 26-MAY-1994
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 07/701,514
 FILING DATE: 16-MAY-1991
 ATTORNEY/AGENT INFORMATION:
 NAME: Matthew P. Vincent
 REGISTRATION NUMBER: 36,709
 REFERENCE DOCKET NUMBER: MIL-004C
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (617) 227-7400
 TELEFAX: (617) 227-5941

INFORMATION FOR SEQ ID NO: 20:

SEQUENCE CHARACTERISTICS:
 LENGTH: 295 amino acids
 TYPE: amino acid
 STRANDEDNESS: Single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide

US-08-246-361A-20

Query Match 3.6%; Score 11; DB 2; Length 295;
 Best Local Similarity 100.0%; Pred. No. 0.017;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 101 LAMNYLDRFLS 111
 Db 80 LAMNYLDRFLS 90

Search completed: March 23, 2004, 16:49:05
 Job time: 25 secs

Query Match 3.6%; Score 11; DB 2; Length 295;
 Best Local Similarity 100.0%; Pred. No. 0.017;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 101 LAMNYLDRFLS 111
 Db 80 LAMNYLDRFLS 90

US-08-246-361A-19

RESULT 15
 US 08-246-361A-20
 Sequence 20, Application US/08246361A
 Patient No. 599882
 GENERAL INFORMATION:
 APPLICANT: BEACH, David H.
 TITLE OF INVENTION: D-TYPE CYCLIN AND USES RELATED THERETO
 NUMBER OF SEQUENCES: 50
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: LAHIVE & COCKFIELD
 STREET: 60 State Street

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OM protein - protein search, using SW model

Run on:

March 23, 2004, 16:48:19 ; Search time 46 Seconds

(without alignments)

Scoring table: OLIGO Gapext 60.0 , Gapext 60.0

Title: Perfect score: US-09-530-209A-2

Sequence: 1 MABENELUSLCTESNVDE..... SACCFSFKTHDSSSYTHLS 308

Scoring table: OLIGO Gapext 60.0 , Gapext 60.0

Searched: 1049977 seqs, 258955339 residues

Word size : 0

Total number of hits satisfying chosen parameters:

1049977

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Published_Applications_AA:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	13	4.2	354	15 US-10-388-269-2
2	12	3.9	349	15 US-10-310-154-426
3	11	3.6	36	14 US-10-199-820-241
4	11	3.6	129	12 US-10-424-599-183234
5	11	3.6	276	15 US-10-424-599-183234
6	11	3.6	295	15 US-10-295-027-636
7	11	3.6	323	12 US-10-425-114-38749
8	11	3.6	348	14 US-10-320-230-12
9	11	3.6	358	15 US-10-409-701-5
10	11	3.6	385	15 US-10-264-049-2598
11	10	3.2	254	9 US-09-778-227A-53
12	10	3.2	289	9 US-09-919-97-54
13	10	3.2	289	13 US-10-024-066-2
14	10	3.2	289	13 US-10-024-066-4

ALIGNMENTS

RESULT 1
US-10-388-269-2
; Sequence 2, Application US/10388269
; Publication No. US20030221221A1
; GENERAL INFORMATION:
; APPLICANT: MURRAY, James Augustus Henry
; TITLE OF INVENTION: PLANTS WITH MODIFIED GROWTH
; FILE REFERENCE: 2121-0151P
; CURRENT APPLICATION NUMBER: US/10/388,269
; CURRENT FILING DATE: 2003-03-12
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 354
; TYPE: PRT
; ORGANISM: Nicotiana tabacum
; US-10-388-269-2

Query Match Similarity 4.2%; Score 13; DB 15; Length 354;
Best Local Similarity 100.0%; Pred. No. 0.00078; Mismatches 0; Indels 0; Gaps 0;

Qy	Db	Matches	Length	Conservative	Mismatches	Indels	Gaps
124 QLLAVACLSLAAK	142 QLLAVACLSLAAK	136	154	13	0	0	0

RESULT 2
US-10-310-154-426
; Sequence 426, Application US/10310154
; Publication No. US20030233670A1
; GENERAL INFORMATION:
; APPLICANT: Edgerton, Michael D
; APPLICANT: Chomet, Paul S.
; APPLICANT: Adams, Thomas H
; APPLICANT: Ruff, Thomas G.
; APPLICANT: Agarwal, Ameeta K.
; APPLICANT: Ahrens, Jeffrey E.

APPLICANT: Ball, James A.
 APPLICANT: Barnu, G.
 APPLICANT: Bell, Erin
 APPLICANT: Bodupalli, Raghava
 APPLICANT: Deikman, Jill
 APPLICANT: Deng, Molian
 APPLICANT: Dong, Jinzhuo
 APPLICANT: Durf, Stephen M.
 APPLICANT: Galligan, Meghan M.
 APPLICANT: Hinchev, Brenda S.
 APPLICANT: Huang, Shihshieh
 APPLICANT: Johnson, G. Richard
 APPLICANT: Jung, Vincent
 APPLICANT: Kretzmer, Keith A.
 APPLICANT: Lai, Chao-Qiang
 APPLICANT: Lee, Galy
 APPLICANT: Lin, Jie-Yi
 APPLICANT: Liu, Jingdong
 APPLICANT: Lu, Bin
 APPLICANT: Luethy, Michael M.
 APPLICANT: Lund, Adrian
 APPLICANT: Madison, Linda L.
 APPLICANT: Mailly, Kathleen A.
 APPLICANT: McKiel, Christine L.
 APPLICANT: Miller, Philip W.
 APPLICANT: Padmavathi, Manchikanti
 APPLICANT: Parnell, Laurence D.
 APPLICANT: Start, William G.
 APPLICANT: Teenesen, Dan
 APPLICANT: Vidya, K.R.
 APPLICANT: Wang, Haiyan
 APPLICANT: Xin, Zhanguo
 APPLICANT: Xiu, Nanfei
 APPLICANT: Yang, Chunzhi
 APPLICANT: Zeng, Xiaoping
 APPLICANT: Zhang, Qiang
 APPLICANT: Zhao, Yequan
 APPLICANT: Zhou, Li

TITLE OF INVENTION: Gene Sequences and Uses Thereof in Plants

FILE REFERENCE: 38-15(52796)B

CURRENT APPLICATION NUMBER: US/10/310,154

CURRENT FILING DATE: 2002-12-04

PRIOR APPLICATION NUMBER: 60/337,358

PRIOR FILING DATE: 2001-12-04

NUMBER OF SEQ ID NOS: 736

SEQ ID NO: 426

LENGTH: 349

TYPE: PRT

ORGANISM: Zea mays

US-10-310-154-426

Query Match 3.9%; Score 12; DB 15; Length 349;
 Best Local Similarity 100.0%; Pred No. 0.0071; Mismatches 0; Indels 0; Gaps 0;

Matches 12; Conservative 0; MisMatches 0; Indels 0; Gaps 0;

QY 125 LLAVATSLAAK 136
 Db 150 LLAVATSLAAK 161

RESULT 3
 US-10-199-820-241
 ; Sequence 241, Application US/10199820
 ; Publication No. US20030180739A1

GENERAL INFORMATION:
 ; APPLICANT: Board of Trustees of the University of Illinois
 ; APPLICANT: Primiano, Thomas
 ; APPLICANT: Chang, Bey-dih
 ; APPLICANT: Robinson, Igor
 ; TITLE OF INVENTION: Methods and Reagents for Identifying Gene Targets for Treating Ca

CURRENT APPLICATION NUMBER: US/10/199,820

CURRENT FILING DATE: 2002-09-23

NUMBER OF SEQ ID NOS: 314

SOFTWARE: PatentIn version 3.0

SEQ ID NO: 241

LENGTH: 36

TYPE: PRT

ORGANISM: Homo sapiens

US-10-199-820-241

Query Match 3.6%; Score 11; DB 14; Length 36;
 Best Local Similarity 100.0%; Pred. No. 0.0082; Mismatches 0; Indels 0; Gaps 0;

Matches 11; Conservative 0; MisMatches 0; Indels 0; Gaps 0;

QY 101 LAMNYDRFLS 111
 Db 25 LAMNYDRFLS 35

RESULT 4
 US-10-424-599-183234
 ; Sequence 183234, Application US/10424599
 ; Publication No. US20040031072A1

GENERAL INFORMATION:
 ; APPLICANT: La Rosa Thomas J
 ; APPLICANT: Kovacic David K
 ; APPLICANT: Zhou Yihua
 ; APPLICANT: Cao Yongwei

TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With FILE REFERENCE: 38-21(53223)B

CURRENT APPLICATION NUMBER: US/10/424,599

CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 285684

SEQ ID NO 183234

LENGTH: 129

TYPE: PRT

ORGANISM: Glycine max

FEATURE:

OTHER INFORMATION: Clone ID: PAT_MRT3847_136474C.1.pep

US-10-424-599-183234

Query Match 3.6%; Score 11; DB 12; Length 129;
 Best Local Similarity 100.0%; Pred. No. 0.026; Mismatches 0; Indels 0; Gaps 0;

Matches 11; Conservative 0; MisMatches 0; Indels 0; Gaps 0;

QY 218 GIDLEFPERSE 228
 Db 9 GIDLEFPERSE 19

RESULT 5
 US-10-116-275-114
 ; Sequence 114, Application US/10116275
 ; Publication No. US20030211476A1

GENERAL INFORMATION:
 ; APPLICANT: Elan Pharmaceutical Technology
 ; APPLICANT: O'Mahony, Daniel J.
 ; APPLICANT: Bryden, David
 ; APPLICANT: Byrne, Darragh
 ; APPLICANT: Lambkin, Imelda
 ; APPLICANT: Higgins, Lisa

TITLE OF INVENTION: Genetic Analysis of Peyer's Patches and M Cells and Methods and Compositions Targeting Peyer's Patches and M Cell Receptors

FILE REFERENCE: E1067-20087

CURRENT APPLICATION NUMBER: US/10/116,275

CURRENT FILING DATE: 2002-10-04

NUMBER OF SEQ ID NOS: 349

SOFTWARE: PatentIn version 3.1

SEQ ID NO: 114

LENGTH: 276

TYPE: PRT

ORGANISM: Homo sapiens

US-10-116-275-114

Query Match 3.6%; Score 11; DB 15; Length 276;
 Best Local Similarity 100.0%; Pred. No. 0.053; Mismatches 0; Indels 0; Gaps 0;

QY 101 LAMNYLDRFLS 111
 Db 80 LAMNYLDRFLS 90

RESULT 6
 US-10-295-027-636
 ; Sequence 636, Application US/10295027
 Publication No. US20030232350A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Afar, Daniel
 ; APPLICANT: Aziz, Natasha
 ; APPLICANT: Ginsberg, Wendy M.
 ; APPLICANT: Gish, Kurt C.
 ; APPLICANT: Glynn, Richard
 ; APPLICANT: Hevezi, Peter A.
 ; APPLICANT: Mack, David H.
 ; APPLICANT: Murray, Richard
 ; APPLICANT: Watson, Susan R.
 ; APPLICANT: Bos Biotechnology, Inc.
 TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and
 TITLE OF INVENTION: Methods of Screening for Modulators of Cancer
 FILE REFERENCE: 018501-012500US
 CURRENT APPLICATION NUMBER: US/10/295,027
 CURRENT FILING DATE: 2002-11-13
 PRIOR APPLICATION NUMBER: US 09/663,733
 PRIOR FILING DATE: 2000-09-15
 PRIOR APPLICATION NUMBER: US 60/350,666
 PRIOR FILING DATE: 2001-11-13
 PRIOR APPLICATION NUMBER: US 60/335,394
 PRIOR FILING DATE: 2001-11-15
 PRIOR APPLICATION NUMBER: US 60/332,464
 PRIOR FILING DATE: 2001-11-21
 PRIOR APPLICATION NUMBER: US 60/334,393
 PRIOR FILING DATE: 2001-11-29
 PRIOR APPLICATION NUMBER: US 60/340,376
 PRIOR FILING DATE: 2001-12-14
 PRIOR APPLICATION NUMBER: US 60/347,211
 PRIOR FILING DATE: 2002-01-08
 PRIOR APPLICATION NUMBER: US 60/347,349
 PRIOR FILING DATE: 2002-01-10
 PRIOR APPLICATION NUMBER: US 60/355,250
 PRIOR FILING DATE: 2002-02-08
 PRIOR APPLICATION NUMBER: US 60/356,714
 PRIOR FILING DATE: 2002-02-13
 Remaining Prior Application data removed - See File Wrapper or PALM.
 NUMBER OF SEQ ID NOS: 1386
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO 635
 LENGTH: 295
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-10-295-027-636

Query Match 3.6%; Score 11; DB 15; Length 295;
 Best Local Similarity 100.0%; Pred. No. 0.056; Mismatches 0; Indels 0; Gaps 0;

QY 101 LAMNYLDRFLS 111
 Db 80 LAMNYLDRFLS 90

RESULT 7
 US-10-425-114-38749
 ; Sequence 38749, Application US/10425114
 ; Publication No. US2003034888A1
 ; GENERAL INFORMATION:

QY 101 LAMNYLDRFLS 111
 Db 80 LAMNYLDRFLS 90

RESULT 8
 US-10-320-230-2
 ; Sequence 2, Application US/10320230
 ; Publication No. US20030110529A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Low, Keith S.
 ; APPLICANT: Tao, Yumin
 ; APPLICANT: Gordon-Kamm, William J.
 ; APPLICANT: Gregory, Carolyn A.
 ; APPLICANT: McElver, John A.
 ; APPLICANT: Hoerter, George J.
 TITLE OF INVENTION: Cyclin D Polynucleotides, Polypeptides
 TITLE OF INVENTION: and Methods of Use
 FILE REFERENCE: 0926D
 CURRENT APPLICATION NUMBER: US/10/320,230
 CURRENT FILING DATE: 2002-12-16
 PRIOR APPLICATION NUMBER: 60/101,551
 PRIOR FILING DATE: 1998-09-23
 PRIOR APPLICATION NUMBER: 09/398,858
 PRIOR FILING DATE: 1999-09-20
 NUMBER OF SEQ ID NOS: 30
 SOFTWARE: FastSEQ for Windows Version 3.0
 SEQ ID NO 2
 LENGTH: 358
 TYPE: PRT
 ORGANISM: Zea mays
 US-10-320-230-2

Query Match 3.6%; Score 11; DB 14; Length 358;
 Best Local Similarity 100.0%; Pred. No. 0.067; Mismatches 0; Indels 0; Gaps 0;

QY 124 QLLAVACLSLA 134
 Db 148 QLLAVACLSLA 158

RESULT 9
 US-10-320-230-12
 ; Sequence 12, Application US/10320230
 ; Publication No. US20030110529A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Low, Keith S.
 ; APPLICANT: Tao, Yumin

APPLICANT: Gordon-Kamm, William J.
 APPLICANT: Gregory, Carolyn A.
 APPLICANT: McElver, John A.
 APPLICANT: Hoerster, George J.
 TITLE OF INVENTION: Cyclin D Polynucleotides, Polypeptides
 FILE REFERENCE: 0920D
 CURRENT APPLICATION NUMBER: US/10/320,230
 CURRENT FILING DATE: 2002-12-16
 PRIOR APPLICATION NUMBER: 6/0/101,551
 PRIOR FILING DATE: 1998-09-23
 PRIOR APPLICATION NUMBER: 09/398,858
 PRIOR FILING DATE: 1999-09-20
 NUMBER OF SEQ ID NOS: 30
 SEQ ID NO: 12
 LENGTH: 358
 TYPE: PRT
 ORGANISM: Zea mays
 /US-10-320-230-12

Query Match 3.6%; Score 11; DB 14; Length 358;
 Best Local Similarity 100.0%; Pred. No. 0.067; Mismatches 0; Indels 0; Gaps 0;
 Matches 11; Conservative 0; Number of SEQ ID NOS: 158
 Qy 124 OLLAVACSLA 134
 Db 148 OLLAVACSLA 158

RESULT 10
 US-10-409-701-5
 ; Sequence 5, Application US/10409701
 ; Publication No. US/0030221224A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Zinselmier, Chris
 ; APPLICANT: Holentirari, Timothy G.
 ; TITLE OF INVENTION: Enhanced Silk Exsertion Under Stress
 ; FILE REFERENCE: 1421.
 ; CURRENT APPLICATION NUMBER: US/10/409,701
 ; CURRENT FILING DATE: 2003-04-08
 ; PRIOR APPLICATION NUMBER: US 6/0/370,796
 ; PRIOR FILING DATE: 2002-04-08
 ; NUMBER OF SEQ ID NOS: 25
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO: 5
 ; LENGTH: 358
 ; TYPE: PRT
 ; ORGANISM: Zea mays
 ; US-10-409-701-5

Query Match 3.6%; Score 11; DB 15; Length 358;
 Best Local Similarity 100.0%; Pred. No. 0.071; Mismatches 0; Indels 0; Gaps 0;
 Matches 11; Conservative 0; Number of SEQ ID NOS: 158
 Qy 101 LAMNYDRFLS 111
 Db 170 LAMNYDRFLS 180

RESULT 12
 US-09-778-927A-53
 ; Sequence 53, Application US/09778927A
 ; Patent No. US/0020068342A1
 ; GENERAL INFORMATION:
 ; APPLICANT: KROSTAVI, Rami et al.
 ; TITLE OF INVENTION: NOVEL NUCLEIC ACID AND AMINO ACID SEQUENCES AND NOVEL
 ; FILE REFERENCE: 2786-0160
 ; CURRENT APPLICATION NUMBER: US/09/778,927A
 ; CURRENT FILING DATE: 2001-02-08
 ; PRIOR APPLICATION NUMBER: IL 134453
 ; PRIOR FILING DATE: 2000-02-09
 ; PRIOR APPLICATION NUMBER: IL135341
 ; PRIOR FILING DATE: 2000-03-29
 ; NUMBER OF SEQ ID NOS: 81
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO: 53
 ; LENGTH: 254
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: misc_feature
 ; LOCATION: (1)..(254)
 ; OTHER INFORMATION: Xaa = any amino acid, unknown, or other
 ; US-09-778-927A-53

Query Match 3.2%; Score 10; DB 9; Length 254;
 Best Local Similarity 100.0%; Pred. No. 0.45; Mismatches 0; Indels 0; Gaps 0;
 Matches 10; Conservative 0; Number of SEQ ID NOS: 88
 Qy 101 LAMNYDRFL 110
 Db 79 LAMNYDRFL 88

RESULT 11
 US-10-264-049-2598
 ; Sequence 2598, Application US/10264049
 ; Publication No. US/20040005579A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Birse et al.
 ; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
 ; FILE REFERENCE: PA133P1
 ; CURRENT APPLICATION NUMBER: US/10/264,049
 ; CURRENT FILING DATE: 2002-10-04
 ; PRIOR APPLICATION NUMBER: PCT/US01/18569
 ; PRIOR FILING DATE: 2001-06-07
 ; PRIOR APPLICATION NUMBER: US 6/0/209,467

RESULT 13
 US-09-319-497-54
 ; Sequence 54, Application US/09919497
 ; Patent No. US/0020106662A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Matter, George L.
 ; TITLE OF INVENTION: PROGNOSTIC CLASSIFICATION OF ENDOMETRIAL CANCER
 ; FILE REFERENCE: B0801/725
 ; CURRENT APPLICATION NUMBER: US/09/919,497
 ; CURRENT FILING DATE: 2001-07-31
 ; PRIOR APPLICATION NUMBER: US 6/0/221,735

PRIOR FILING DATE: 2000-07-31
 NUMBER OF SEQ ID NOS: 100
 SOFTWARE: PatentIn version 3.0
 SEQ ID NO 54
 LENGTH: 289
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-09-919-497-54

Query Match 3.2%; Score 10; DB 9; Length 289;
 Best Local Similarity 100.0%; Pred. No. 0.51; Mismatches 0; Indels 0; Gaps 0;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 101 LAMNYLDRFL 110
 Db 79 LAMNYLDRFL 88

US-10-024-066-4
 Query Match 3.2%; Score 10; DB 13; Length 289;
 Best Local Similarity 100.0%; Pred. No. 0.51; Mismatches 0; Indels 0; Gaps 0;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 101 LAMNYLDRFL 110
 Db 79 LAMNYLDRFL 88

RESULT 14

US-10-024-066-2

; Sequence 2, Application US/10024066
 ; Publication No. US2002016613A1

; GENERAL INFORMATION:

; APPLICANT: Field, Loren J.

; ATTORNEY/AGENT: Pasumarthi, Kishore Babu S.

; TITLE OF INVENTION: CARDIOMYOCYTES WITH ENHANCED PROLIFERATIVE POTENTIAL,

; TITLE OF INVENTION: AND METHODS FOR PREPARING AND USING SAME

; FILE REFERENCE: 7037-450

; CURRENT APPLICATION NUMBER: US/10/024, 066

; CURRENT FILING DATE: 2001-12-18

; PRIOR APPLICATION NUMBER: PCT/US00/16827

; PRIOR FILING DATE: 2000-06-19

; NUMBER OF SEQ ID NOS: 8

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 2

; LENGTH: 289

; TYPE: PRT

; ORGANISM: Mus musculus

; US-10-024-066-2

RESULT 15

US-10-024-066-4

; Sequence 4, Application US/10024066
 ; Publication No. US2002016613A1

; GENERAL INFORMATION:

; APPLICANT: Field, Loren J.

; ATTORNEY/AGENT: Pasumarthi, Kishore Babu S.

; TITLE OF INVENTION: CARDIOMYOCYTES WITH ENHANCED PROLIFERATIVE POTENTIAL,

; TITLE OF INVENTION: AND METHODS FOR PREPARING AND USING SAME

; FILE REFERENCE: 7037-450

; CURRENT APPLICATION NUMBER: US/10/024, 066

; CURRENT FILING DATE: 2001-12-18

; PRIOR APPLICATION NUMBER: 60/139, 942

; PRIOR FILING DATE: 1999-06-18

; PRIOR APPLICATION NUMBER: PCT/US00/16827

; PRIOR FILING DATE: 2000-06-19

; NUMBER OF SEQ ID NOS: 8

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 4

; LENGTH: 289

; TYPE: PRT

; ORGANISM: Homo sapiens

search completed: March 23, 2004, 16:53:55
 Job time : 53 SECs

GenCore version 5.1.6
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Om protein - protein search, using sw model

Run on:

March 23, 2004, 16:44:27 ; Search time 21 Seconds

(without alignments)

1410.809 Million cell updates/sec

Title: US-09-530-209a-2
Perfect score: 308
Sequence: 1 MABENLBSILCLESNVVDE.....SACCFSRKHDSSSSYTHLS 308
Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 283366 seqs, 96191526 residues

Word size : 0

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

PIR 78:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	DB ID	Description
1	20	6.5	317	T49995 cyclin protein-like - Arabidopsis thaliana
2	13	4.2	334	S51650 cyclin delta-1 - A
3	13	4.2	339	A98725 hypothetical prote
4	12	3.9	291	S51922 cyclin D1 - Africa
5	12	3.9	291	S62720 cyclin D1 - zebra
6	11	3.6	295	A39977 cyclin D1 - human
7	11	3.6	295	A55523 cyclin D1 - mouse
8	11	3.6	295	JC2342 cyclin D1 - rat
9	11	3.6	418	S11678 cyclin D2 - African
10	10	3.2	288	2 JC011 cyclin D2 - rat
11	10	3.2	288	2 JC011 cyclin D2 - rat
12	10	3.2	289	2 A11984 cyclin D2 - mouse
13	10	3.2	289	2 A42822 cyclin D2 - human
14	10	3.2	291	2 JC5759 cyclin D2 - chicken
15	9	2.9	291	2 S77925 cyclin D2 - Africa
16	9	2.9	321	2 T04720 hypothetical prote
17	9	2.9	372	2 T03961 cyclin D-like prote
18	9	2.9	376	2 T05420 cyclin delta-3 - A
19	8	2.6	178	2 T28035 cyclin D-like prote
20	8	2.6	237	2 C40035 hypothetical prote
21	8	2.6	263	2 T00397 hypothetical prote
22	8	2.6	292	2 B42822 cyclin D3 - human
23	8	2.6	293	2 JC012 cyclin D3 - rat
24	8	2.6	300	1 A62444 thioredoxin-disulf
25	8	2.6	302	1 E85041 probable D-type cy
26	8	2.6	318	1 D23766 nodulin protein
27	8	2.6	328	2 B83271 hypothetical prote
28	8	2.6	361	2 CB4613 probable cyclin D
29	8	2.6	361	2 T45860 cyclin D3-like pro

ALIGNMENTS

RESULT 1							
T49995	cyclin protein-like - Arabidopsis thaliana						
N	Alternate name: Protein P12B17.210						
C;Species:	Arabidopsis thaliana (mouse-ear cress)						
C;Date:	02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 02-Jun-2000						
C;Accession:	T4995						
R;Bevan, M.; Bancroft, I.; Meves, H.W.; Rudd, S.; Lemcke, K.; Mayer, K.F.X.							
submitted to the Protein Sequence Database, April 2000							
A;Reference number: 225026							
A;Accession: T49995							
A;Status: Preliminary							
A;Molecule type: DNA							
A;Residues: 1-317 <EBV>							
A;Cross-references: EMBL:ALL353995; GSPDB:GN00063; ATSP:F12B17.210							
C;Genetic:							
A;Gene: ATSP:F12B17.210							
A;Map position: 5							
A;Introns: 78/3; 107/3; 140/3; 221/3; 266/3							
Query Match	5.5%	Score	20;	DB	2;	Length	317;
Best Local Similarity	100.0%	Pred.	No.	3.2e-12;	Indels	0;	Gaps
Matches	20;	Conservative	0;	Mismatches	0;		
OY	100	CLAMNLYDRFLSVHDPSGK	119				
Db	91	CLAMNLYDRFLSVHDPSGK	110				

RESULT 2							
S51650	cyclin delta-1 - Arabidopsis thaliana						
C;Species:	Arabidopsis thaliana (mouse-ear cress)						
C;Date:	07-May-1995 #sequence_revision 21-Jul-1995 #text_change 09-Sep-1997						
C;Accession:	S51650						
R;Soni, R.; Carmichael, J.P.; Shah, Z.H.; Murray, J.A.H.							
submitted to the EMBL Data Library, December 1994							
A;Description: A family of cyclin D homologs from plants differentially controlled by 9							
A;Reference number: S51650							
A;Accession: S51650							
A;Molecule type: mRNA							
A;Residues: 1-34 <SON>							
A;Cross-references: EMBL:X83369; NID:g603504; PID:g603505							
C;Keywords: cell cycle control; cell division control							
Query Match	4.2%	Score	13;	DB	2;	Length	334;
Best Local Similarity	100.0%	Pred.	No.	5.2e-05;	Indels	0;	Gaps
Matches	13;	Conservative	0;	Mismatches	0;		
OY	124	QIIVAVACSLAAK	136				

Db 128 ||||||| QLLAVACLSLAAK 140

Biochim. Biophys. Acta 1264, 257-260, 1995
A;Title: Zebrafish cyclin D1 is differentially expressed during early embryogenesis.

A;Reference number: S62730; MUID:96138542; PMID:8947308

RESULT 3

A96725

hypothetical protein F9P5_7 [imported] - Arabidopsis thaliana

C;Species: Arabidopsis thaliana (mouse-ear cress)

C;Accession: A96725 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-291 <YAR>

A;Cross-references: EMBL:X87581; NID:gi143440; PIDN:CAA60885_1; PID:gi143441

A;Note: the source is designated as *Danio rerio*

C;Superfamily: cyclin

Query Match Best Local Similarity 3.9%; Score 12; DB 2; Length 291; Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY ||||| 101 LAMNYLDRLFSV 112

Db 80 LAMNYLDRLFSV 91

RESULT 6

A8977

cyclin D1 - human

N;Alternate names: cyclin BCL1; cyclin D; PRAD1; probable bcl-1 transforming protein

C;Species: Homo sapiens (man)

C;Date: 27-Mar-1996 #sequence_revision 12-Apr-1996 #text_change 16-Jul-1999

C;Accession: A38977; A41523; S14794; A40034; B40268; S51701; I54032; S42495

R;Kimokni, R.; Berger, F.; Bastard, C.; Klein, B.; French, M.; Archimbaud, E.; Rouault, T.;

Blood 83, 3689-3696, 1994

A;Title: Rearrangement of CCND1 (BCL1/PRAD1) 3' untranslated region in mantle-cell lymphoma

A;Reference number: A38977; MUID:94284323; PMID:8204893

A;Accession: A38977

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-295 <RIM>

A;Cross-references: GB:Z23022; NID:gi312911; PIDN:CAA80558_1; PID:gi312912

R;Witers, D.A.; Harvey, R.C.; Faust, J.B.; Melnyk, O.; Carey, K.; Meeker, T.C.

Mol. Cell. Biol. 11, 4846-4853, 1991

A;Title: Characterization of a candidate bcl-1 gene.

A;Reference number: A41523; MUID:92017758; PMID:1833629

A;Accession: A41523

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-295 <WIT>

A;Cross-references: GB:M73554; NID:gi179364; PIDN:CAA58392_1; PID:gi179365

R;Motokura, T.; Bloom, T.; Kim, H.G.; Jueppner, H.; Ruderman, J.V.; Kronenberg, H.M.;

Nature 350, 512-515, 1991

A;Title: A novel cyclin encoded by a bcl1-linked candidate oncogene.

A;Reference number: S14794; MUID:91194766; PMID:1865542

A;Accession: S14794

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-295 <WOT>

A;Cross-references: EMBL:X59798; NID:gi935631; PIDN:CAA42470_1; PID:gi35632

R;Xiong, Y.; Connolly, T.; Putcher, B.; Beach, D.

Cell 65, 691-699, 1991

A;Title: Human D-type cyclin

A;Reference number: A40034; MUID:91235304; PMID:1827756

A;Accession: A40034

A;Molecule type: mRNA

A;Residues: 1-129, 'G', 131-187, 'S', 189-295 <X10>

A;Cross-references: GB:MG6449; NID:gi81244; PIDN:AAA52136_1; PID:gi81245

A;Note: the authors translated the codon TCT for residue 188 as Leu

R;Lew, D.J.; Dulic, V.; Reed, S.I.

Cell 66, 1197-1206, 1991

A;Title: Isolation of three novel human cyclins by rescue of G1 cyclin (Cln) function

A;Reference number: A40268

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-167, 'I', 170-295 <LEW>

A;Cross-references: GB:M74092

R;Alberti, S.; Stella, M.; Dell'Arciprete, R.; Bucci, C.; Nutini, M.; Naglieri, A.M.; submitted to the EMBL Data Library, February 1994

Db

101 LAMNYLDRLFSV 112

78 LAMNYLDRLFSV 89

RESULT 5

S62730

cyclin D1 - zebra fish

C;Species: Brachydanio rerio (zebra fish)

C;Date: 24-Aug-1996 #sequence_revision 13-Mar-1997 #text_change 20-Jun-2000

C;Accession: S62730

R;Yarden, A.; Salomon, D.; Geiger, B.

A;Reference number: S51700
A;Accession: S51701
A;Status: preliminary
A;Molecule type: mRNA
A;Cross-references: EMBL:X77754
R;Motokura, T.; Arnold, A.
Genes Chromosomes Cancer 7, 89-95, 1993
A;Title: The PRAD1/cyclin D1 proto-oncogene: Genomic organization, 5' DNA sequence, and
A;Reference number: 154082; MUID:93326527; PMID:687458
A;Accession: 154082
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-66 <REBS>
A;Cross-references: GB:L09054; NID:9307344; PIDN:AAA36481.1; PID:9307345
C;Genetics:
A;Gene: GDB:CCND1; PRAD1; DI1S28
A;Cross-references: GDB:128222; OMIM:168461
A;Note: this gene either contains or is contiguous to GDB:BCL1
C;Superfamily: cyclin
C;Keywords: cell cycle control; proto-oncogene

Query Match 3.6%; Score 11; DB 2; Length 295;
Best Local Similarity 100.0%; Pred. No. 0.0053; Mismatches 11; Conservative 0; Indels 0; Gaps 0;
Matches 11; Conservatve 0; Mismatches 0; Indels 0; Gaps 0;
QY 101 LAMNYLDRLFS 111
Db 80 LAMNYLDRLFS 90

RESULT 7

A5523
cyclin D1 - mouse
C;Species: Mus musculus (house mouse)
C;Accession: 21-Jul-1995 #sequence_revision 28-Jul-1995 #text_change 16-Jul-1999
C;Accession: A5523; A4035
R;Smith, R.; Peters, G.; Dickson, C.
Genom 25, 85-2, 1995
A;Title: Genomic organization of the mouse cyclin D1 gene (Cyl-1).
A;Reference number: A5523; MUID:95293413; PMID:774359
A;Accession: A5523
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-295 <SMI>
A;Cross-references: GB:578355; NID:994896; PIDN:AAB24495.1; PMID:994897
R;Matsushime, H.; Rousset, M.F.; Ashmun, R.A.; Sherr, C.J.
Cell, 70, 701-713, 1991
A;Title: Colony-stimulating factor 1 regulates novel cyclins during the G1 phase of the
A;Reference number: A40035; MUID:91235305; PMID:1827757
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-295 <MAT>
A;Cross-references: GB:M64403; NID:912877; PIDN:AAA37502.1; PID:912878
C;Superfamily: cyclin
C;Keywords: cell cycle control

RESULT 8

Query Match 3.6%; Score 11; DB 2; Length 295;
Best Local Similarity 100.0%; Pred. No. 0.0053; Mismatches 11; Conservative 0; Indels 0; Gaps 0;
Matches 11; Conservatve 0; Mismatches 0; Indels 0; Gaps 0;
QY 101 LAMNYLDRLFS 111
Db 80 LAMNYLDRLFS 90

RESULT 8

JCC342
cyclin D1 - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 16-Jul-1999
C;Accession: JC342
R;Hosokawa, Y.; Osga, T.; Nakashima, K.
Gene 147, 249-252, 1994
A;Title: Induction of D2 and D3 cyclin-encoding genes during promotion of the G1/S transition by cyclin D1
A;Reference number: JC342; MUID:95011623; PMID:792609
A;Accession: JC342
A;Molecule type: mRNA
A;Residues: 1-288 <HOS>
A;Cross-references: GB:D16308; NID:9577334; PIDN:BA03815.1; PID:9577335
A;Experimental source: Nb2 cell
A;Note: The authors translated the codon GAA for residue 68 as Glu, TGC for residue 104 as

C;Accession: JC2342; S44147
R;Blanchi, S.; Fabiani, S.; Muratori, M.; Arnold, A.; Sakaguchi, K.; Miki, T.; Brandi, R;Biochem. Biophys. Res. Commun. 204, 691-700, 1994
A;Title: Calcium modulates the cyclin D1 expression in a rat parathyroid cell line.
A;Reference number: JC2342; MUID:95071382; PMID:7980531
A;Accession: JC2342
A;Molecule type: mRNA
A;Residues: 1-295 <BI1>
A;Cross-references: EMBL:X75207; NID:9473122; PIDN:CAA53020.1; PID:9473123
A;Experimental source: epithelial parathyroid cell line
R;Blanchi, S.; Fabiani, S.; Muratori, M.; Sakaguchi, K.; Arnold, A.; Miki, T.; Brandi submitted to the EMBL Data Library, September 1993
A;Description: Cloning and calcium regulation of cyclin D1 gene in a rat parathyroid cell line
A;Reference number: S44147
A;Accession: S44147
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-295 <BI2>
A;Cross-references: EMBL:X75207; NID:9473122; PIDN:CAA53020.1; PID:9473123
C;Superfamily: cyclin
C;Keywords: cell cycle control

RESULT 9

S11678
cyclin A - African clawed frog
C;Species: Xenopus laevis (African clawed frog)
C;Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 16-Jul-1999
C;Accession: S11678
R;Minshull, J.; Golsteyn, R.; Hill, C.S.; Hunt, T.
EMBO J. 9, 2665-2675, 1990
A;Title: The A- and B-type cyclin associated cdc2 kinases in Xenopus turn on and off a
A;Reference number: S11678; MUID:90360999; PMID:2143983
A;Accession: S11678
A;Molecule type: mRNA
A;Residues: 1-418 <MIN>
A;Cross-references: EMBL:X53745; NID:964644; PIDN:CAA37775.1; PID:964645
A;Residues: 1-418 <MIN>
C;Superfamily: cyclin
C;Keywords: cell cycle control

RESULT 10

Query Match 3.6%; Score 11; DB 2; Length 418;
Best Local Similarity 100.0%; Pred. No. 0.0073; Mismatches 11; Conservative 0; Indels 0; Gaps 0;
Matches 11; Conservatve 0; Mismatches 0; Indels 0; Gaps 0;
QY 101 LAMNYLDRLFS 111
Db 220 LAMNYLDRLFS 230

JC4011
cyclin D2 - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 13-Jun-1995 #sequence_revision 14-Jul-1995 #text_change 20-Jun-2000
C;Accession: JC4011
R;Hosokawa, Y.; Osga, T.; Nakashima, K.
Gene 147, 249-252, 1994
A;Title: Induction of D2 and D3 cyclin-encoding genes during promotion of the G1/S transition by cyclin D1
A;Reference number: JC4011; MUID:95011623; PMID:792609
A;Accession: JC4011
A;Molecule type: mRNA
A;Residues: 1-288 <HOS>
A;Cross-references: GB:D16308; NID:9577334; PIDN:BA03815.1; PID:9577335
A;Experimental source: Nb2 cell
A;Note: The authors translated the codon GAA for residue 68 as Glu, TGC for residue 104 as

C;Genetics:
A;Gene: d2
C;Superfamily: cyclin
C;Keywords: cell cycle control

Query Match 3.2%; Score 10; DB 2; Length 288;
Best Local Similarity 100.0%; Pred. No. 0.055; Mismatches 0; Indels 0; Gaps 0;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 101 LAMNYLDRFL 110
Db 78 LAMNYLDRFL 87

RESULT 13
A42822
cyclin D2 - human
cyclin D2 - Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 16-Jul-1999
C;Accession: A42822; 137268; A42821; S2680
R;Xiong, Y.; Meuninger, J.; Beach, D.; Ward, D.C.
Genomics 13, 575-584, 1992
A;Title: Molecular cloning and chromosomal mapping of CCND genes encoding human D-type
A;Accession: 158372
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-288 <RES>
A;Reference number: 158372; MUID:9327561; PMID:8502486
A;Cross-references: GB:MM90913; NID:9179999; PIDN:AA51925_1; PID:9180000
A;Cross-references: GB:M90913; NID:9179999; PIDN:AA51925_1; PID:9180000
A;Note: Sequence extracted from NCBI Backbone (NCBIN:10963; NCBIG:10965)
A;Palmero, I.; Holder, A.; Sinclair, A.J.; Dickson, C.; Peters, G.
Oncogene 8, 1049-1054, 1993
A;Title: Cyclins D1 and D2 are differentially expressed in human B-lymphoid cell lines
A;Reference number: 137268; MUID:93205384; PMID:845931
A;Accession: 137268
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-289 <RES>
A;Cross-references: EMBL:X69452; NID:934815; PIDN:CA48493_1; PID:938415
A;Cross-references: EMBL:X69452; NID:934815; PIDN:CA48493_1; PID:938415
R;Imaba, T.; Matsushime, H.; Valentine, M.; Roussel, M.F.; Sherr, C.J.; Look, A.T.
Genomics 13, 565-574, 1992
A;Title: Genomic organization, chromosomal localization, and independent expression of
A;Accession: A42821
A;Reference number: A42821; MUID:92347850; PMID:1386335
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-165, 'NV', 168-223, 'H', 225-240 <RES>
A;Cross-references: GB:MB8093; NID:9180008; PIDN:AA51928_1; PID:9180010
A;Genetics:
A;Gene: GDB:CCND2
A;Cross-references: GDB:128968; OMIM:123833
A;Map position: 12P13-12P13
C;Superfamily: cyclin
C;Keywords: cell cycle control

Query Match 3.2%; Score 10; DB 2; Length 289;
Best Local Similarity 100.0%; Pred. No. 0.055; Mismatches 0; Indels 0; Gaps 0;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 101 LAMNYLDRFL 110
Db 79 LAMNYLDRFL 88

RESULT 14
JC4579
cyclin D2 - chicken
cyclin D2 - Cyl D2
N;Alternate names: Cyl D2
C;Species: Gallus gallus (chicken)
C;Date: 08-Mar-1995 #sequence_revision 19-Apr-1996 #text_change 31-Mar-2000
C;Accession: JC4579
C;Cross-references: GB:MB6182
A;Accession: JC4579
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 54-289 <RES>
A;Cross-references: GB:MB6182
C;Superfamily: cyclin
C;Keywords: cell cycle control

Query Match 3.2%; Score 10; DB 2; Length 289;
Best Local Similarity 100.0%; Pred. No. 0.055; Mismatches 0; Indels 0; Gaps 0;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 101 LAMNYLDRFL 110
Db 78 LAMNYLDRFL 87

RESULT 15
JC4579
cyclin D2 - chicken
cyclin D2 - Cyl D2
N;Alternate names: Cyl D2
C;Species: Gallus gallus (chicken)
C;Date: 08-Mar-1995 #sequence_revision 19-Apr-1996 #text_change 31-Mar-2000
C;Accession: JC4579
C;Cross-references: GB:MB6182
A;Accession: JC4579
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-291 <RES>

A;Cross-references: GB:U28900; NID:9968968; PIDN:AAA96955.1; PID:9968969
 A;Experimental source: UG9 T-cell
 C;Comment: This protein acts as a regulator of the cell-cycle-dependent proteinkinase gene product, binds to these products in a combinatorial fashion, activates their enzyme activity
 C;Genetics:
 A;Gene: cyl2
 C;Superfamily: cyclin
 C;Keywords: cell cycle control

F,29-193/Region: cyclin-box similarity

Query Match 3.2%; Score 10; DB 2; Length 291;
 Best Local Similarity 100.0%; Pred. No. 0 055; Mismatches 0; Indels 0; Gaps 0;
 Matches 10; Conservative 0; N mismatches 0; I ndels 0; G aps 0;
 Qy 101 LAMNYLDRFL 110
 Db 79 LAMNYLDRFL 88

RESULT 15

S57925

cyclin D2 - African clawed frog

C;Species: Xenopus laevis (African clawed frog)

C;Date: 13-Jan-1996 #sequence_revision 12-Apr-1996 #text_change 16-Jul-1999

C;Accession: S57925; S51681

R;Cockerill, M.J.; Hunt, T.

submitted to the EMBL Data Library, July 1995

A;Description: D-type cyclins in Xenopus laevis.

A;Reference number: S57922

A;Accession: S57925

A;Molecule type: mRNA

A;Residues: 1-291 <COC>

A;Cross-references: EMBL:X89476; NID:9897820; PIDN:CAA61665.1; PID:9897821

R;Taieb, F.; Jesus, C.

submitted to the EMBL Data Library, December 1994

A;Reference number: S51681

A;Accession: S51681

A;Molecule type: mRNA

A;Residues: 1-291 <TAI>

A;Cross-references: EMBL:X83503; NID:9603899; PIDN:CAA58493.1; PID:9603900

C;Superfamily: cyclin

C;Keywords: cell cycle control

Query Match 2.9%; Score 9; DB 2; Length 291;

Best Local Similarity 100.0%; Pred. No. 0 59; Mismatches 0; Indels 0; Gaps 0;

Matches 9; Conservative 0; N mismatches 0; I ndels 0; G aps 0;

Qy 102 AMNYLDRFL 110

Db 80 AMNYLDRFL 88

Search completed: March 23, 2004, 16:48:29
 Job time : 23 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model.

Run on: March 23, 2004, 16:40:35 ; Search time 18 Seconds
(without alignments)

890.978 Million cell updates/sec

Title: US-09-530-209A-2

Perfect score: 308

Sequence: 1 MAEENELSLICTESSNVDE.....SACCFSPKTHDSSSSYTHLS 308

Scoring table: ORIGO Gapop 60.0 , Gapext 60.0

Searched: 141681 seqs, 52070155 residues

Word size : 0

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database : SwissProt_42;*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	13	4.2	335	1 CGD1_ARATH
2	12	3.9	291	1 CGD1_BRARE
3	12	3.9	291	1 CGD1_XENIA
4	12	3.6	292	1 CGD1_CHICK
5	11	3.6	295	1 CGD1_HUMAN
6	11	3.6	295	1 CGD1_MOUSE
7	11	3.6	295	1 CGD1_RAT
8	11	3.6	418	1 CGD1_XENLA
9	10	3.2	288	1 CGD2_RAT
10	10	3.2	289	1 CGD2_HUMAN
11	10	3.2	289	1 CGD2_MOUSE
12	10	3.2	291	1 CGD2_CHICK
13	9	2.9	291	1 CGD2_XENIA
14	9	2.9	376	1 CGD3_ARATH
15	8	2.5	292	1 CGD3_HUMAN
16	8	2.6	292	1 CGD3_MOUSE
17	8	2.6	293	1 CGD3_RAT
18	8	2.6	318	1 NODD_RALIT
19	8	2.6	361	1 CGD2_ARATH
20	8	2.6	382	1 CGB2_ORYUJA
21	8	2.6	391	1 CGA1_CARAJI
22	8	2.6	542	1 XPS5_STRLT
23	8	2.6	1375	1 RPOB_COXBU
24	8	2.6	1468	1 FMBB_AQUAE
25	7	2.3	104	1 GLRK_VERFO
26	7	2.3	1 PHP1_MOUSE	
27	7	2.3	220	1 REHY_ORYSA
28	7	2.3	233	1 B915_XENLA
29	7	2.3	240	1 ATP7_ARATH
30	7	2.3	244	1 FIMB_BORPE
31	7	2.3	246	1 PHBB_CHRVT
32	7	2.3	251	1 GLO2_BUCAU
33	7	2.3	251	1 Y137_CHLNP

ALIGNMENTS				
CGD1_ARATH	RN	CGD1_ARATH	STANDARD;	PRT; 335 AA.
ID	CGD1_ARATH	ID	CGD1_ARATH	PRT; 335 AA.
PA2751;	004525;	PA2751;	004525;	
DT	01-NOV-1995 (rel. 32, Created)	DT	15-DEC-1998 (rel. 37, Last sequence update)	
DT	28-FEB-2003 (rel. 41, Last annotation update)	DE	Cyclin delta-1.	
DE	Cyclin delta-1.	GN	CYCCL1 OR ATG70210 OR F20P5_7.	
OS	Eukaryota; Viridiplantae; Streptophyta; Embryophyta;	OC	Spermaphyta; Magnoliophyta; eudicots; Brassicae; Arabidopsis.	
OC	eurosidae II; Brassicales; Arabidopsis.	OX	NCBI_TaxID=3702;	
RN	[1]	RN	SEQUENCE FROM N.A.	
RC	STRAIN=cv. Landsberg erecta; TISSUE=Seedling;	RA	Soni R.; Carmichael J.P.; Shah Z.H.; Murray J.A.H.;	
RA	"A family of cyclin D homologs from plants differentially controlled by growth regulators and containing the conserved retinoblastoma protein interaction motif.";	RA	RT	
RT	RT	RT	RT	
RL	RT	RL	RT	
RP	REVISED.	RP	RP	
RA	Murray J.A.H.;	RA	Medline ID=21016719; PubMed=11130712;	
RA	Submitted (MAR-1998) to the EMBL/GenBank/DDJB databases.	RA	Theologis A., Becker J.R., Palm C.J., Federer N.A., Kaul S., White O., Alonso J., Altzafri B., Aravio R., Bowman C.L., Brooks S.Y., Buehler E., Chan A., Chao Q., Chen H., Cheuk R.F., Chin C.W., Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K., Dunn P., Etgu P., Feilday T.V., Feng J.-D., Fong B., Fujii C.Y., Gill J.E., Goldsmith A.D., Haas B., Hansen N.F., Hughes B., Huizar L., Hunter J.L., Jenkins J., Johnson-Hobson C., Khan S., Khaykin E., Kim C.J., Koo H.L., Kremenevskaya I., Kurtz D.B., Kwan A., Lam B., Langin-Hooper S., Lee A., Lee J.M., Lenz C.A., Li J.H., Li Y.-P., Lin X., Liu S.X., Liu Z.A., Luos J.S., Maiti R., Marziali A., Mittscher J., Miranda M., Ngwen M., Neerman W.C., Osborne B.I., Pai G., Peterson J., Pham P.K., Rizzo M., Rooney T., Rowley D., Sahao H., Salzberg S.L., Schwartz J.R., Shin H., Southwick A.M., Sun H., Tallon L.J., Tambang G., Toriumi M.J., Town C.D., Utterback T., Van Aken S., Vaynberg M., Vysotskaya V.S., Walker M., Wu D., Yu G., Fraser C.M., Venter J.C., Davis R.W., "Sequence and analysis of chromosome 1 of the plant Arabidopsis thaliana.";	
RA	Nature 408:816-820 (2000)	RL	Nature 408:816-820 (2000)	
CC	-1-SIMILARITY: Belongs to the cyclin family. Cyclin D subfamily.	CC	O9czj1 mus musculus	
CC		CC	Q8dmP synchococcus	
CC		CC	Q66119 cucumber mo	
CC		CC	Q62680 mycobacteri	
CC		CC	Q24006 lantimicro	
CC		CC	Q9Ydm5 aeropyrum p	
CC		CC	Q55147 syncrhocyst	
CC		CC	Q8lyc oryza sativ	
CC		CC	P0183 arabidopsis	
CC		CC	P03396 watsonia an	
CC		CC	Q81bp arabidopsis	
CC		CC	P09137 bacillus su	

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DR EMBL; X83369; CRA58285.1; -.

DR EMBL; AC002062; AAB61096.1; -.

DR PIR; A96725; AS6725.

DR InterPro; IPR06670; Cyclin.

DR InterPro; IPR04367; Cyclin_Cterm.

DR InterPro; IPR06671; Cyclin_N.

DR Pfam; PF00134; cyclin_1.

DR Pfam; PF00284; cyclin_C_1.

DR SMART; SM00385; CYCLIN_1.

DR PROSITE; PS00092; CYCLIN_1.

KW Cyclin; Cell cycle; Cell division; Multigene family.

FT CONFLICT 313 313 S -> SRSSS (IN RBP. 3.)

SEQUENCE 335 AA; 37868 MW; D365767F3D2FC339 CRC64;

Oy 124 QLLAVACSLAAK 136 4.2%; Score 13; DB 1; Length 335;
 Best Local Similarity 100.0%; Pred. No. 0.0001; Mismatches 0; Indels 0; Gaps 0;
 Matches 13; Conservative 0; MisMatches 0; IndelS 0; Gaps 0;

Dy 128 QLLAVACSLAAK 140

RESULT 2

ID	CGDL_BRARE	STANDARD	PRT	291 AA.
AC	Q90459;			
DT	15-JUL-1998 (Rel. 36, Created)			
DT	15-JUL-1998 (Rel. 36, Last sequence update)			
DT	28-FEB-2003 (Rel. 41, Last annotation update)			
DE	G1/S-specific cyclin D1.			
GN	CND1 OR CYC1			
OS	Brachydanio rerio (Zebrafish) (Danio rerio).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;			
OC	Cyprinidae; Danio.			
OX	NCBI_TAXID=7955;			
RN	[1]			
RP	SIMQUENCE FROM N.A.			
RX	Medline:96118542; PubMed:83747308;			
RA	Yarden A., Salomon D., Geiger B.;			
RT	"Zebrafish cyclin D1 is differentially expressed during early embryogenesis.";			
RL	Biochim. Biophys. Acta 1264:257-260(1995).			
CC	-!- FUNCTION: Essential for the control of the cell cycle at the G1/S (start) transition.			
CC	-!- SUBUNIT: Interacts with the CDK4 and CDK6 protein kinases to form a serine/threonine kinase holoenzyme complex. The cyclin subunit			
CC	-!- IMPARTS Substrate specificity to the complex.			
CC	-!- SIMILARITY: Belongs to the cyclin family. Cyclin D subfamily.			
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CC	DR EMBL; X83751; CAA0885.1; -.			
DR PIR; S62730; S62730.				
DR ZFIN; ZDB-GENE-980526-176; cond1.				
DR InterPro; IPR004367; Cyclin_Cterm.				
DR InterPro; IPR006671; Cyclin_N.				
DR Pfam; PF00134; cyclin_1.				
DR Pfam; PF00284; cyclin_C_1.				
DR SMART; SM00385; CYCLIN_1.				
DR SMART; PS00092; CYCLIN_1.				

```

KW Cycin; Cell Cycle; Cell division.
SQ CYCIN: Cell Cycle; Cell division.

Query Match 3.9%; Score 12; DB 1; Length 291;
Best Local Similarity 100.0%; Pred. No. 0.00084; Mismatches 0; Indels 0; Gaps 0;
Matches 12; Conservative 0; MisMatches 0; Indexes 0; DEGaps 0;

Qy 101 LAMNYLDREFLSV 112
  ||||| | | | | |
Db 80 LAMNYLDREFLSV 91
  ||||| | | | | |

RESULT 3
CGD1_XENIA STANDARD PRT; 291 AA.
ID CGD1_XENIA
AC P50755;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE G1/S-specific cyclin D1.
GN CND1.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
OC Xenopodina; Xenopus.
NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RA Cockrell M.J.; Hunt T. ;
RL Submitted (JUN-1995) to the EMBL/GenBank/DBJ databases.
CC -I- FUNCTION: Essential for the control of the cell cycle at the G1/S
  (start) transition.
CC -I- SUBUNIT: Interacts with the CDK4 and CDK5 protein kinases to form
  a serine/threonine kinase holoenzyme complex. The cyclin subunit
  imparts substrate specificity to the complex.
CC -I- SIMILARITY: Belongs to the cyclin family. Cyclin D subfamily.
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  or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X89475; CAB61644; 1; .
DR PIR; S57922; S57922.
DR Intero; IPR006670; Cyclin.
DR Interpro; IPR004367; Cyclin_Cterm.
DR InterPro; IPR006671; Cyclin_N.
DR Pfam; PF00134; cyclin_1.
DR Pfam; PF02984; cyclin_C_1.
DR SMART; SM00385; CYCLIN_1.
DR PROSITE; PS00292; CYCLINS_1.
DR Cycillin; Cell_cycle; Cell_division; Multigene_family.
SQ SEQUENCE 291 AA; 32953 MW; A4747C5BD1679087 CRC64;
  ||||| | | | | |
Query Match 3.9%; Score 12; DB 1; Length 291;
Best Local Similarity 100.0%; Pred. No. 0.00084; Mismatches 0; Indels 0; Gaps 0;
Matches 12; Conservative 0; MisMatches 0; Indexes 0; DEGaps 0;

Qy 101 LAMNYLDREFLSV 112
  ||||| | | | | |
Db 78 LAMNYLDREFLSV 89
  ||||| | | | | |

```

DR G1/S-specific cyclin D1.
 GN CNDL
 RN Gallus gallus (Chicken).
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OX NCBI_TaxID=9031;
 RN SEQUENCE FROM N.A.
 [1] RA Li H., Lahti J.M., Kidd V.J.;
 RA Submitted (DEC-1995) to the EMBL/GenBank/DBJ databases.
 CC -I- FUNCTION: Essential for the control of the cell cycle at the G1/S
 (start) transition. Interacts with the CDK4 and CDK6 protein
 kinases (By similarity).
 -I- SIMILARITY: Belongs to the cyclin family. Cyclin D subfamily.
 CC
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 or send an email to license@isb-sib.ch).
 CC
 DR EMBL; U40844; AAH32711.1; --.
 DR InterPro; IPR00292; Cyclin; Cyclin_Cterm.
 DR InterPro; IPR00436; Cyclin_N.
 DR Pfam; PF00134; cyclin; 1.
 DR Pfam; PF02894; cyclin_C; 1.
 DR SMART; SM00385; CYCLIN; 1.
 DR PROSITE; PS00292; CYCLINS; 1.
 KW Cyclin; Cell Cycle; Cell division; Multigene family.
 SQ SBQUENCE 292 AA; 33263 MW; 7B543029DB45A67D CRC64;
 Query Match Best Local Similarity 3.6%; Score 11; DB 1; Length 292;
 Matches 100.0%; Pred. No. 0.078; Mismatches 0; Indels 0; Gaps 0;
 QY 101 LAMYLDPLS 111
 DB 80 LAMYLDPLRS 90
 RESULT 5
 CGDL_HUMAN STANDARD; PRT; 295 AA.
 ID CGDL_HUMAN STANDARD; PRT; 295 AA.
 AC P24385;
 DT 01-MAR-1992 (Rel. 21, Created)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE G1/S-specific cyclin D1 (PRAD1 oncogene) (BCL-1 oncogene).
 GN CNDL OR PRAD1 OR BCL1.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 RN NCBI_TaxID=9606;
 RN SEQUENCE FROM N.A.
 [1] RX MEDLINE=91194766; PubMed=1826542;
 RX MEDLINE=91194766; PubMed=1826542;
 RX MEDLINE=91194766; PubMed=1826542;
 RX MEDLINE=91194766; PubMed=1826542;
 RN "A novel cyclin encoded by a bcl1-linked candidate oncogene.";
 RN Nature 350:512-515(1991).
 RN [2] RX SEQUENCE FROM N.A.
 RX MEDLINE=92005671; PubMed=1833066;
 RA Lew D.J., Dulic V., Reed S.T.;
 RT "Isolation of three novel human cyclins by rescue of G1 cyclin (Cln)
 function in yeast";
 RL Cell 66:1197-1206(1991).
 RN [3] RX SEQUENCE FROM N.A.
 RN
 RX MEDLINE=9123534; PubMed=1827756;
 RA Xilong Y., Connolly T., Futcher B., Beach D.;
 RT "Human D-type cyclin.";
 RL Cell 65:691-699(1991).
 RN [4] RX MEDLINE=9201778; PubMed=1833629;
 RA Withers D.A., Harvey R.C., Faust J.B., Melnyk O., Carey K.,
 Meeker T.C.;
 RT "Characterization of a candidate bcl-1 gene.";
 RL Mol. Cell. Biol. 11:4846-4853(1991).
 RN [5] RX MEDLINE=9201778; PubMed=1833629;
 RA Rimokh R., Berger F., Bastard C., Klein B., French M., Archimbaud E.,
 Rouault J.-P., Santa Lucia B., Duret L., Vuillaume M.;
 RT "Rearrangement of CNDL(BCL1/PRAD1) 3' untranslated region in
 mantle-cell lymphomas and t(11q13)-associated leukemias.";
 RL Blood 83:3689-3696(1994).
 RN [6] RX SEQUENCE FROM N.A.
 RA Riedel M.J., Livingston R.J.J., Daniels M.R., Montoya M.A., Chung M.-W.,
 RA Miyamoto K.E., Nguyen C.P., Neuyen D.A., Poel C.L., Robertson P.D.,
 RA Schachwitz W.S., Sherwood J.K., Wirak L.A., Nickerson D.A.;
 RA Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
 RN [7] RX SEQUENCE FROM N.A.
 RC TISSUE=Brain; and Placenta;
 RX STRauberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D.,
 RA Klausner R.D., Colline F.S., Wagner J., Shemer C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Bustoff K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marsina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiruki S., Carninci P., Prange C.J.,
 RA Raha S.S., Logeland N.A., Peters G.J., Abramson R.D., Mullally S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muniz M.F., Sodegran J.J., Lin X., Gibbs R.A.,
 RA Fahay J., Heitton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakely R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
 RA Schnurch A., Schein J.E., Jones S.J.M., Marrs M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 human and mouse cDNA sequences";
 RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [8] RX INTERACTION WITH CDK4 AND CDK6.
 RX MEDLINE=9413440; PubMed=3302605;
 RA Bates S., Bonetta L., McAllan D., Parry D., Holder A., Dickson C.,
 RA Peters G.;
 RT "CDK6 (PLSTRE) and CDK4 (PSK-T3) are a distinct subset of the
 cyclin-dependent kinases that associate with cyclin D1.";
 RT Oncogene 9:71-79(1994).
 CC -I- FUNCTION: Essential for the control of the cell cycle at the G1/S
 (start) transition.
 CC -I- SUBUNIT: Interacts with the CDK4 and CDK6 protein kinases to form
 CC a serine/threonine kinase holoenzyme complex. The cyclin subunit
 CC imparts substrate specificity to the complex.
 CC -I- DISEASE: Involved in B-Lymphocytic malignancy (particularly
 CC mantle-cell lymphoma (MCL)) by a chromosomal translocation
 CC (t(11q14)(q13;q32)) that involves CNDL and immunoglobulin gene
 CC regions (BCL1 oncogene). Activation of CNDL may be oncogenic by
 CC directly altering progression through the cell cycle.
 CC -I- DISEASE: Involved in a subset of parathyroid adenomas by a
 CC chromosomal translocation t(11q11.1)(q13;p15) that involves CNDL
 CC and the parathyroid hormone (PTH) enhancer (PRAD1 oncogene).
 CC -I- SIMILARITY: Belongs to the cyclin family. Cyclin D subfamily.
 CC -I- DATABASE: NAME=Atlas Genet. Cytogenet. Oncol. Haematol.;
 CC WWW="<http://www.infobiogen.fr/services/chromcancer/genes/BCL1.html>".

AC P39948; 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last Sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE GI/S-specific cyclin D1.

GN CND1.

OS *Rattus norvegicus* (Rat).
OC Eukaryota; Chordata; Craniata; Vertebrata; Buteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
RN [1] NCBITaxID=10116;

RP SEQUENCE FROM N.A.

RC TISSUE-Kidney; TISSUE-Ovary;

RX MEDLINE=93330551; PubMed=8336937;
RA Tamura K., Kanoaka Y., Janno S., Nagata A., Ogiso Y., Shimizu K., Hayakawa T., Nojima H., Okayama H.;
RA "Cyclin G: a new mammalian cyclin with homology to fission yeast Cig1.";
RL Oncogene 8:2113-2118(1993).
RN [2]

RP SEQUENCE FROM N.A.;
RX MEDLINE=95071382; PubMed=7980531;
RA Bianchi S., Fabiani S., Muratori M., Arnold A., Sakaguchi K., Miki T., Brandi M.L.;
RT "Calcium modulates the cyclin D1 expression in a rat parathyroid cell line.";
RL Biochem. Biophys. Res. Commun. 204:691-700(1994);
CC -!- FUNCTION: Essential for the control of the cell cycle at the G1/S (start) transition. Interacts with the CDK4 and CDK6 protein kinases.
CC -!- SIMILARITY: Belongs to the cyclin family. Cyclin D subfamily.
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CC -!- SIMILARITY: Belongs to the cyclin family. Cyclin AB subfamily.
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CC -!- SIMILARITY: Belongs to the cyclin family. Cyclin AB subfamily.
CC DR EMBL; X5207; CAA33020.1; -.
DR PIR; X5207; JC2342.
DR InterPro; IPR006670; Cyclin.
DR InterPro; IPR004367; Cyclin_Cterm.
DR Pfam; PF00134; cyclin_1.
DR Pfam; PF02984; cyclin_C_1.
DR SMART; SM00385; CYCLIN_2.
DR PROSITE; PS00292; CYCLINS_1.
KW Cyclin; Cell cycle; Cell division; Mitosis.
SQ SEQUENCE 418 AA; 46772 MW; FER0B7A1F801E6A CRC64;

Query Match 3.6%; Score 11; DB 1; Length 418; Best Local Similarity 100.0%; Pred. No. 0.0078; 0; Mismatches 0; Indels 0; Gaps 0; Matches 11; Conservative 0; MisMatches 0; Indels 0; Gaps 0;

QY 101 LAMNYLDRRLS 111
Db 220 LAMNYLDRRLS 230

RESULT 9

CGD2_RAT CGD2_RAT STANDARD; PRT; 288 AA.
ID CGD2_RAT
AC QP4827;
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE GI/S-specific cyclin D2 (Vin-1 proto-oncogene).
GN CCND2 OR VIN-1.
OS *Rattus norvegicus* (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
RN [1] NCBITaxID=10116;

RP SEQUENCE FROM N.A.;
RX MEDLINE=9327561; PubMed=8502486;
RA Hama Z., Jankowski M., Tremblay P., Jiang X.M., Milatovich A., Francke U., Jolicœur P.;
RT "The Vin-1 gene, identified by provirus insertional mutagenesis, is the cyclin D2;"
RT Oncogene 8:1661-1666(1993).
RN [2]

RP SEQUENCE FROM N.A.
 RX MEDLINE=95011623; PubMed=7926809;
 RA Hosokawa Y., Onga T., Nakashima K.;
 RT "Induction of D2 and D3 cyclin-encoding genes during promotion of the
 GL/S transition by prolatin in rat Nb2 cells.";
 RL Gene 147:249-252 (1994).
 -!- FUNCTION: Essential for the control of the cell cycle at the G1/S
 (start) transition.
 -!- SUBUNIT: Interacts with the CDK4 and CDK6 protein kinases to form
 a serine/threonine kinase holoenzyme complex. The cyclin subunit
 imparts substrate specificity to the complex.
 CC -!- SIMILARITY: Belongs to the Cyclin family. Cyclin D subfamily.

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 or send an email to license@isb-sib.ch).

 CC EMBL; D09752; AAA41010.1; -.
 CC EMBL; D16308; BAA0815.1; -.
 DR PIR: 158372; 158372.
 DR PIR; JG4011; JC4011.
 DR InterPro; IPR006670; Cyclin.
 DR InterPro; IPR004367; Cyclin_Cterm.
 DR InterPro; IPR006671; Cyclin_N.
 DR Pfam; PF00134; cyclin; 1.
 DR Pfam; PF02984; cyclin_C; 1.
 DR SMART; SM00385; Cyclin_N; 1.
 DR PROSITE; PS00592; CYCLINS_1.
 KW Cyclin; Cell cycle; Cell division; Multigene family; Proto-oncogene.
 FT CONFLICT 68 68 E -> G (IN REF. 2).
 FT CONFLICT 104 104 C -> V (IN REF. 2).
 FT CONFLICT 232 232 T -> A (IN REF. 2).
 SQ SEQUENCE 288 AA; 32826 MW; 4B322BFE983FC1 CRC64;
 Query Match 3.2%; Score 10; DB 1; Length 288;
 Best Local Similarity 100.0%; Pred. No. 0.071; 0; Mismatches 0; Indels 0; Gaps 0;
 Matches 10; Conservative 0; Misplaced 0;
 Qy 101 LAMNYLDRL 110
 Db 78 LAMNYLDRL 87

 RESULT 10
 CGD2_HUMAN STANDARD; PRT; 289 AA.
 ID P30279; Q03955; (Rel. 25, Created)
 DT 01-APR-1993 (Rel. 25, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE G1/S-specific cyclin D2.
 GN CCND2.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1] SEQUENCE FROM N.A.
 RP MEDLINE=92347851; PubMed=1386335;
 RX MEDLINE=92347851; PubMed=1386335;
 RA Inaba T., Matsushime H., Valentine M., Roussel M.F., Sherr C.J.,
 RT "Genomic organization, chromosomal localization, and independent
 expression of human cyclin D genes.",
 RL Genomics 13:565-574 (1992).
 CC -!- FUNCTION: Essential for the control of the cell cycle at the G1/S
 (start) transition.
 -!- SUBUNIT: Interacts with the CDK4 and CDK6 protein kinases to form
 a serine/threonine kinase holoenzyme complex. The cyclin subunit
 imparts substrate specificity to the complex.
 CC -!- SIMILARITY: Belongs to the cyclin family. Cyclin D subfamily.

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 or send an email to license@isb-sib.ch).

 CC EMBL; M90813; AAA51926.1; -.
 DR EMBL; X69452; CAA8493.1; -.
 DR EMBL; D13639; BAA02802.1; -.
 DR EMBL; AFS18005; AAM54041.1; -.
 DR EMBL; BC010958; AAI10958.1; -.
 DR EMBL; M88083; AAA51928.1; -.
 DR EMBL; M88080; AAA51928.1; JOINED.
 DR EMBL; M88081; AAA51928.1; JOINED.
 DR EMBL; M88082; AAA51928.1; JOINED.
 DR PIR; A42822; A42822.
 DR Gener; HGNC:11883; CCND2.
 DR GK; P30279; -.
 DR MM; 123933; -.
 DR InterPro; IPR006670; Cyclin.

DR InterPro; IPR004367; Cyclin_Cterm.
 DR InterPro; IPR006651; Cyclin_N.
 DR Pfam; PF00134; cyclin; 1.
 DR SMART; SM00385; CYCLIN; 1.
 DR PROSITE; PS00292; CYCLINS; 1.
 KW Cyclin; Cell cycle; Cell division; Multigene family.
 KW KU -> NV (IN REF. 6).
 FT CONFLICT 156 224 T -> H (IN REF. 6).
 FT CONFLICT 157 224 T -> H (IN REF. 6).
 SEQUENCE 289 AA; 33067 MW; E4EFEBF476D76D90 CRC64;

Query Match 3.2%; Score 10; DB 1; Length 289;
 Best Local Similarity 100.0%; Pred. No. 0.071; Length 289;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 101 LAMNYLDRFL 110
 DB 79 LAMNYLDRFL 88

RESULT 11

CGD2_MOUSE	STANDARD;	PRT;	289 AA.
ID P30280;			
AC			
DT 01-APR-1993 (Rel. 25, Created)			
DT 01-APR-1993 (Rel. 25, last sequence update)			
DT 16-OCT-2001 (Rel. 40, Last annotation update)			
DE G1/S-specific cyclin D2.			
GN CCND2 OR CYL-2.			
OS Mus musculus (Mouse).			
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OX Gallus.			
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
RN [1]			
SEQUENCE FROM N.A.			
RP MEDLINE-92198134; PubMed=1372445; RA Kyokawa H., Busquets X., Powell C.T., Ngo L., Rifkind R.A., RT Marks P.A.; RN "Cloning of a D-type cyclin from murine erythrocytoma cells."; RL Proc. Natl. Acad. Sci. U.S.A. 89:2444-2447(1992).			
RP SEQUENCE FROM N.A.			
RA MEDLINE-9123305; PubMed=1627757; RT Matsushime H., Roussel M.F., Ashmun R.A., Sherr C.J.; RL Proc. Natl. Acad. Sci. U.S.A. 89:2444-2447(1992).			
RP SEQUENCE FROM N.A.			
RA Matsushime H., Roussel M.F., Ashmun R.A., Sherr C.J.; RT "Colony-stimulating factor 1 regulates novel cyclins during the G1 phase of the cell cycle."; RL Cell 65:701-713(1991).			
CC --!- FUNCTION: Essential for the control of the cell cycle at the G1/S (S130T) transition.			
CC --!- SUBUNIT: Interacts with the CDK4 and CDK6 protein kinases to form a serine/threonine kinase holoenzyme complex. The cyclin subunit imparts substrate specificity to the complex.			
CC --!- SIMILARITY: Belongs to the cyclin family. Cyclin D subfamily.			
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CC DR EMBL; U28980; AAC99555.1; -.			
CC DR PIR; J4579; JC4579.			
CC DR InterPro; IPR006670; Cyclin.			
CC DR InterPro; IPR004367; Cyclin_Cterm.			
CC DR InterPro; IPR006671; Cyclin_N.			
CC DR Pfam; PF00134; cyclin; 1.			
CC DR SMART; SM00385; CYCLIN; 1.			
CC DR PROSITE; PS00292; CYCLINS; 1.			
CC KW Cyclin; Cell cycle; Cell division; Multigene family.			
CC KW GO:GO00074; Regulation of cell cycle; IMP.			
CC DR InterPro; IPR006670; Cyclin.			
CC DR InterPro; IPR004367; Cyclin_Cterm.			
CC DR InterPro; IPR006671; Cyclin_N.			
CC DR Pfam; PF00134; cyclin; 1.			
CC DR SMART; SM00385; CYCLIN; 1.			
CGD2_XENIA	STANDARD;	PRT;	291 AA.
ID CGD2_XENIA			
AC P53782;			

DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last Sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE GL1/S-specific cyclin D2.
 GN CCND2.
 OS *Xenopus laevis* (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
 OC Xenopodinae; Xenopus.
 NCBI_TaxID=8355;
 RN [1] RA
 RP SEQUENCE FROM N.A.
 RA Cockerill M.J.; Hunt T.;
 RL Submitted (JUL-1995) to the EMBL/GenBank/DBJ databases.
 RN [2] RP
 SEQENCE FROM N.A.
 RX MEDLINE-97380591; PubMed=9237366;
 RA Tariq F.; Jezzard C.;
 RT "Xenopus cyclin D2: cloning and expression in oocytes and during early development"; Biol. Cell 88:99-111(1996).
 CC !- FUNCTION: Essential for the control of the cell cycle at the GL1/S (start) transition.
 CC !- SUBUNIT: Interacts with the CDK4 and CDK6 protein kinases to form a serine/threonine kinase holoenzym complex. The cyclin subunit
 CC imparts substrate specificity to the complex.
 CC !- SIMILARITY: Belongs to the Cyclin family.
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 CC
 CC EMBL; X83476; CAA61665.1; --.
 DR EMBL; X83503; CAA54931.1; --.
 PRT; S57925; S57925.
 DR InterPro; IPR006670; Cyclin.
 DR InterPro; IPR004367; Cyclin_Cterm.
 DR InterPro; IPR006671; Cyclin_N.
 DR Pfam; PF0134; Cyclin_1.
 DR Pfam; PF02984; cyclin_C_1.
 PROSITE; PS00385; CYCLIN_1.
 DR CYCLIN; Cell_cycle; Cell_division; Multigene_family.
 KW SEQUENCE 291 AA; 32959 MW; 94290F04F1531E89 CRC64;
 Query Match 2.9%; Score 9; DB 1; Length 291;
 Best Local Similarity 100.0%; Pred. No. 0.66;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 102 AMNYLDRL 110
 DB B0 AMNYLDRL 88
 RESULT 14
 CGD3_ARATH STANDARD:
 ID CGD3_ARATH PRT: 376 AA.
 AC P42753; C049489;
 DT 01-Nov-1995 (Rel. 32, Created)
 DT 15-Dec-1998 (Rel. 37, Last sequence update)
 DT 10-Oct-2003 (Rel. 42, Last annotation update)
 DE Cyclin delta-3.
 GN CYCD3 OR AT4G34160 OR F28A23.80.
 OS *Arabidopsis thaliana* (Mouse-ear cress).
 OC Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 OC NCBI_TaxID=3702;
 RN [1] RA
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV. Landsberg erecta; TISSUE-Seeding;
 RX MEDLINE=95210930; PubMed=7696891;
 RA Soni R.; Carmichael J.P.; Shah Z.H.; Murray J.A.H.;
 RT "A family of cyclin D homologs from plants differentially controlled by growth regulators and containing the conserved retinoblastoma protein interaction motif"; Plant Cell 7:85-103 (1995).
 RL [2] RP
 REVISION TO 371.
 RA Murray J.A.H.; Wedell H.; Ridley P.;
 RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ database.
 RN [3] RP
 SEQENCE FROM N.A.
 RC STRAIN=CV. Columbia;
 RX MEDLINE=20033488; PubMed=10617198;
 RA Mayer K.F.X.; Schueler C.; Wambutt R.; Murphy G.; Volckaert G.;
 RA Pohl T.; Duesterhoeft A.; Stiekema W.; Entian K.-D.; Terry N.;
 RA Harris B.; Ansorge W.; Brandt P.; Grivell L.A.; Rieger M.;
 RA Weichselgarner M.; de Simone V.; Obermaier B.; Mache R.; Mueller M.;
 RA Kreis M.; Del Seny M.; Puigdomenech P.; Watson M.; Schmidtheini T.';
 RA Reichert B.; Portetelle D.; Perez-Alonso M.; Boutry M.; Bancroft I.;
 RA Vos P.; Hoheisel J.; Zimmermann W.; Wedell H.; Ridley P.;
 RA Langham S.-A.; McCullagh B.; Blaham L.; Robben J.;
 RA Van der Schueren J.; Grymonpre B.; Chuang Y.-J.; Vandenhussche F.;
 RA Bracken M.; Weltjens I.; Voet M.; Bautista I.; Aert R.; Defoor E.;
 RA Witztumger T.; Bothe G.; Ramsperger U.; Hilbert H.; Braun M.;
 RA Holzer B.; Brandt A.; Peters S.; van Staveren M.; Dirks W.;
 RA Moolman P.; Klein Lankhorst R.; Rose M.; Hauf J.; Koetter P.;
 RA Bernreiser S.; Hempel S.; Pelpausch M.; Lambeth S.; van den Daele H.;
 RA De Keyser A.; Burekhaert C.; Gielan J.; Villarreal R.; De Clercq R.;
 RA Van Montagu M.; Rogers J.; Cronin A.; Quail M.A.; Bray-Aiken S.;
 RA Clark J.; Doogert J.; Hall S.; Kay M.; Leonard N.; McLay K.; Mayes R.;
 RA Pettett A.; Rajandream M.A.; Lyne M.; Bense V.; Rechnann S.;
 RA Borrova D.; Bloecker H.; Scharfe M.; Grimm M.; Loehnert T.-H.;
 RA Dose S.; de Haan M.; Maarse A.C.; Schaefer M.; Mueller-Auer S.;
 RA Gabel C.; Ruchs M.; Pitzmann B.; Grandercat K.; Dauer D.; Herzl A.;
 RA Neumann S.; Argiriou A.; Vitale D.; Ligouri R.; Piravandi E.;
 RA Massenet O.; Quideley F.; Clabauid G.; Muendlein A.; Feilber R.;
 RA Schnabl S.; Hiller R.; Schmidt W.; Lecharny A.; Aubourg S.;
 RA Chofford F.; Cooke R.; Berger C.; Monfort A.; Casacuberta E.;
 RA Gibbons T.; Weber N.; Vandembol M.; Bargues M.; Terol J.; Torres A.;
 RA Perez-Perez A.; Purnell D.; Bent E.; Johnson S.; Tacon D.; Jesse J.;
 RA Heijnen L.; Schwarz D.; Scholler P.; Heber S.; France P.; Bielke C.;
 RA Friesman D.; Haase D.; Lemcke K.; Meves H.-W.; Stocker S.;
 RA Zaccaria P.; Bevan M.; Wilson R. K.; de la Bastide M.; Habermann K.;
 RA Parneil L.; Dechka M.; Gnoj L.; Schutz K.; Huang E.; Spiegel L.;
 RA Sekhon M.; Murray J.; Sheet P.; Cordes M.; Abu-Threideh J.;
 RA Stoenking T.; Kalicki J.; Graves T.; Harmon G.; Edwards J.;
 RA Latreille P.; Courtney L.; Cloud J.; Abbott A.; Scott K.; Johnson D.;
 RA Minx P.; Bentley D.; Fulton B.; Miller N.; Greco T.; Kemp K.;
 RA Kramer J.; Fulton L.; Mardis E.; Dante M.; Pepin K.; Hillier L. W.;
 RA Nelson J.; Spieth J.; Ryan E.; Andrews S.; Geisel C.; Layman D.;
 RA Du H.; Ali J.; Berghoff A.; Jones K.; Drone K.; Cotton M.; Joshi C.;
 RA Antoniou B.; Zidianic M.; Strong C.; Sun H.; Lamar B.; Yordan C.;
 RA Ma P.; Zhong J.; Preston R.; Vil D.; Shekher M.; Matero A.; Shah R.;
 RA Swaby I.K.; O'Shaughnessy A.; Rodriguez M.; Hoffman J.; Till S.;
 RA Granat S.; Shochdy N.; Haseeva A.; Hameed A.; Iodhi M.; Johnson A.;
 RA Chen E.; Marra M.A.; Martienssen R.; McCombie W.R.;
 RT "Sequence and analysis of chromosome 4 of the plant *Arabidopsis thaliana*";
 RL Nature 402:769-777(1999).
 CC !- SIMILARITY: Belongs to the cyclin family. Cyclin D subfamily.
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 CC
 DR EMBL; X83371; CAA88287.1; --.

DR EMBL; AL021961; CAA17556.1; "-.
 DR EMBL; AL161584; CAA80133.1; "-.
 DR PIR; T05420; T05420.
 DR InterPro; IPR006670; Cyclin.
 DR InterPro; IPR004337; Cyclin_Cterm.
 DR InterPro; IPR006671; Cyclin_N.
 DR Pfam; PF00134; cyclin_1.
 DR Pfam; PF02984; cyclin_C; 1.
 DR SMART; SM00385; CYCLIN_2.
 DR PROSITE; PS00292; CYCLINS_1.
 KW Cyclin; Cell cycle; Cell division; Multigene family.
 FT CONFLICT; 288
 SEQUENCE 376 AA: 42/47 MW: F88D5B6BC435FAC2 CRC64;
 Query Match 2.9%; Score 9; DB 1; Length 376;
 Best Local Similarity 100.0%; Pred. No. 0.82; Mismatches 0; Indels 0; Gaps 0;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qry 128 VACISLAK 136
 Db 137 VACISLAK 145

RESULT 15
 CGD_HUMAN STANDARD; PRT: 292 AA.
 ID CGD_HUMAN ; STANDARD; PRT: 292 AA.
 AC P0281; Q96F9; (Rel. 25, Created)
 DT 01-APR-1993 (Rel. 41, last sequence update)
 DT 28-FEB-2003 (Rel. 42, last annotation update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE G1/S-specific cyclin D3.
 GN CCND3.
 OS Homo sapiens (Human).
 OC Eukaryota; Chordata; Craniata; Vertebrata; Buteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TAXID=9606;
 RN [1] SEQUENCE FROM N.A., AND VARIANT ALA-259.
 RX MEDLINE:9234851; PubMed=1366336;
 RA Xiong Y.; Meuninger J.; Beach D.C.; Ward D.C.;
 RT "Molecular cloning and chromosomal mapping of cCND genes encoding
 RT human D-type cyclins.";
 RL Genomics 13:575-584(1992).
 RN [2] SEQUENCE FROM N.A.
 RP SEQUENCE FROM N.A., AND VARIANT ALA-259.
 RX MEDLINE:93015922; PubMed=13033201;
 RA Motokura T.; Keyomarsi K.; Kronenberg H.M.; Arnold A.;
 RT "Cloning and characterization of human cyclin D3, a cDNA closely
 related in sequence to the PRAD1(cyclin D1 proto-oncogene);"
 RT J. Biol. Chem. 267:20412-20415(1992).
 J. [3] SEQUENCE FROM N.A., AND VARIANT ALA-259.
 Rieder M.J.; Livingston R.J.; Braun A.C.; Montoya M.A.; Chung M.-W.;
 RA Miyamoto K.E.; Nguyen C.P.; Nguyen D.A.; Poel C.L.; Robertson P.D.;
 RA Schackwitz W.S.; Sherwood J.K.; Witkow D.A.;
 RL Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
 RN [4] SEQUENCE FROM N.A.
 RX TISSUE=gang;
 RA Strausberg R.L.; Feingold E.A.; Grouse L.H.; Derge J.G.;
 RA Klausner R.D.; Collins F.S.; Wagner L.; Shemesh C.M.; Schulter G.D.;
 RA Altschul S.F.; Zeeberg B.; Buetow K.H.; Schaefer C.F.; Blatt N.K.;
 RA Hopkins R.F.; Jordan H.; Moore T.; Max S.I.; Wang J.J.; Hsieh F.;
 RA Ditchko L.; Marusina K.; Farmer A.A.; Rubin G.M.; Hong L.;
 RA Stapleton M.; Soakes M.B.; Bonaldo M.F.; Casavant T.L.; Scheetz T.E.;
 RA Brownstein M.J.; Ustid T.B.; Toshiyuki S.; Carninci P.; Prange C.;
 RA Raha S.S.; Loquellano N.A.; Peters G.J.; Abramson R.D.; Mullany S.J.;
 RA Bosak S.A.; McEwan P.J.; McCormick K.J.; Malek J.A.; Gunaratne P.H.;
 RA Richards K.C.; Hale S.; Garcia A.M.; Gay L.J.; Hulyk S.W.;
 RA Villalon D.K.; Munro D.M.; Sodergren E.J.; Lu X.; Gibbs R.A.;
 RA Fahey J.; Heaton E.; Kettman M.; Madan A.; Rodrigues S.; Sanchez R.;
 RA Whiting M.; Madan A.; Young A.C.; Shevchenko Y.; Bouffard G.G.

RA Blakesley R.W.; Touchman J.W.; Green E.D.; Dickson M.C.;
 RA Rodriguez A.C.; Grimwood J.; Schmutz J.; Myers R.M.;
 RA Butterfield Y.S.N.; Krzywinski M.I.; Skalska U.; Smialus D.E.;
 RA Schenck A.; Schein J.E.; Jones S.J.M.; Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 human and mouse cDNA sequences"; Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [5] SEQUENCE OF 52-237 FROM N.A.
 RT TISSUE=Placenta;
 RX Inaba T.; Matsushime H.; Valentine M.; Roussel M.F.; Sherr C.J.;
 RA Look A.T.; Matsushime H., Valentine M., Roussel M.F., Sherr C.J.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smialus D.E.,
 RA Schenck A., Schein J.E., Jones S.J.M., Marra M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length
 human and mouse cDNA sequences"; Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN SPQUENCE OF 52-237 FROM N.A.
 RT TISSUE=Placenta;
 RL Genomics 13:565-574(1992).
 CC -!- FUNCTION: Essential for the control of the cell cycle at the G1/S
 CC -!- (start) transition.
 CC -!- SUBUNIT: Interacts with the CDK4 and CDK6 protein kinases to form
 CC a serine/threonine kinase holoenzyme complex. The cyclin subunit
 CC -!- SIMILARITY: Belongs to the cyclin family. Cyclin D subfamily.
 CC -!- This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL Outstation
 CC at the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
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 CC entities requires a license agreement (see <http://www.isb-sib.ch/announce/>)
 CC or send an email to license@isb-sib.ch).
 CC -!-
 DR EMBL; M90814; AAAS1927.1; "-.
 DR EMBL; M92287; AAAS2127.1; "-.
 DR EMBL; AF15725; AAAS1826.1; "-.
 DR EMBL; BC011616; AAH161616.1; "-.
 DR EMBL; M88087; AAAS1929.1; JOINED.
 DR EMBL; M88084; AAAS1929.1; JOINED.
 DR EMBL; M88085; AAAS1928.1; JOINED.
 DR EMBL; M88086; AAAS1929.1; JOINED.
 DR PIR; BA2822; BA2822.
 DR Genew; HGNC:1585; CCND3.
 DR GK; P30281; "-.
 DR MIM; 123834; "-.
 DR GO; GO:0000074; P:regulation of cell cycle; TAS.
 DR InterPro; IPR006670; Cyclin.
 DR InterPro; IPR004367; Cyclin_Cterm.
 DR Pfam; PF00134; cyclin_1.
 DR Pfam; PF02984; cyclin_C; 1.
 DR SMART; SM00385; CYCLIN_1.
 DR PROSITE; PS00292; CYCLINS_1.
 KW Cyclin; Cell cycle; Cell division; Polymorphism; Multigene family.
 FT VARIANT 259 AA: 32519 MW: 168781604FB0029 CRC64;
 FT VARIANT 259 AA: 32519 MW: 168781604FB0029 CRC64;
 SEQUENCE 292 AA: 32519 MW: 168781604FB0029 CRC64;
 Query Match 2.6%; Score 8; DB 1; Length 292;
 Best Local Similarity 100.0%; Pred. No. 6.1; Mismatches 0; Indels 0; Gaps 0;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Job time : 37 secs

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OM protein - protein search, using sw model

Run on:

March 23, 2004, 16:43:48 ; Search time 45 Seconds

(without alignments) 2159.547 Million cell updates/sec

Title: US-09-530-209A-2
Perfect score: 308
Sequence: 1 MAEENELSLCTESNVDE.....SACCFSFKTHDSSSYTHLS 308

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 1017041 seqs, 315518202 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

- 1: SPTRNEMBL_25:*
- 2: SP_archea:*
- 3: SP_bacteria:*
- 4: SP_fungi:*
- 5: SP_invertebrate:*
- 6: SP_mammal:*
- 7: SP_mbcl:*
- 8: SP_organelle:*
- 9: SP_phage:*
- 10: SP_plant:*
- 11: SP_rabbit:*
- 12: SP_virus:*
- 13: SP_vertebrate:*
- 14: SP_unclassified:*
- 15: SP_rvirus:*
- 16: SP_bacteriop:*
- 17: SP_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No. Score Query Match Length DB ID Description

1 308 100.0 308 10 Q9XFR7 O9xfrr7 arabiopisis

2 228 74.0 308 10 Q9fkp7 Q9fkp7 abidiopsis

3 171 55.5 308 10 Q8LGL1 Q8lgl arabidopsis

4 20 6.5 317 10 Q9lx96 Q9lx96 arabidopsis

5 13 4.2 354 10 Q9R9X9 Q9rzx9 nicotiana t

6 13 4.2 356 10 Q8BSC0 Q8bsc0 oryza sativ

7 13 4.2 382 10 Q816U0 Q816u0 daucus caro

8 12 3.9 291 13 Q8avQ4 Q8avq4 xenopus lae

9 12 3.9 291 13 Q7ZIJ6 Q7zyj6 xenopus lae

10 12 3.9 291 13 Q8gfp4 Q8gfp4 brachydaniio

11 11 3.6 191 11 Q9nb4 Q9nb4 ratmus norv

12 11 3.6 358 10 Q8524 Q8s524 zea mays (m

13 10 3.2 156 11 Q9D919 Q9d919 mus musculu

14 10 3.2 190 13 Q57481 Q57481 stictostedio

15 10 3.2 343 10 Q9SNV1 Q9snv1 antirrhinum

16 10 3.2 350 10 Q7Xab6 Q7xab6 euphorbia e

17	10	3.2	355	10	Q9XAB7	Q7xab7 euphorbia e
18	9	3.2	371	10	Q84vB8	Q84vb8 populus alb
19	9	2.9	153	13	P79919	P79919 xenopus lae
20	9	2.9	198	10	Q8S521	Q8s521 zea mays (m
21	9	2.9	315	10	Q8GVE0	Q8gve0 helianthus
22	9	2.9	321	10	Q9SZ6	Q9sz6 arabidopsis
23	9	2.9	330	10	Q9SNV2	Q9snv2 antirrhinum
24	9	2.9	349	10	Q82678	Q82678 chenopodium
25	9	2.9	372	10	P93103	P93103 chenopodium
26	9	2.9	390	10	Q8S522	Q8s522 zea mays (m
27	8	2.6	178	5	Q23641	Q23641 caenorhabditis
28	8	2.6	232	17	Q9TB27	Q9tb27 thermoplasm
29	8	2.6	241	2	Q9ACH9	Q9ach9 uncultured
30	8	2.6	241	2	Q9ACT2	Q9act2 uncultured
31	8	2.6	241	2	Q9AE49	Q9ae49 uncultured
32	8	2.6	241	2	Q9AC10	Q9aci0 uncultured
33	8	2.6	241	2	Q9AC14	Q9aci4 uncultured
34	8	2.5	241	2	Q9AE47	Q9ae47 uncultured
35	8	2.5	241	2	Q9AC14	Q9aci4 uncultured
36	8	2.5	241	2	Q9ACH8	Q9ach8 uncultured
37	8	2.5	263	10	Q92156	Q92156 arabidopsis
38	8	2.5	300	17	Q28718	Q28718 archaeoglob
39	8	2.6	302	10	Q9E4G0	Q9e4g0 strongylloce
40	8	2.6	302	10	Q9E4G4	Q9e4g4 leishmania
41	8	2.6	308	10	Q8LPW3	Q8lpw3 helianthus
42	8	2.6	328	16	Q9HZ3	Q9hz3 pseudomonas
43	8	2.6	356	8	Q8LH8	Q8lh8 oryza sativ
44	8	2.6	357	10	Q8GVG9	Q8gvg9 helianthus

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

ALIGNMENTS

RESULT 1

Q9XFR7 ID Q9XFR7 PRELIMINARY; PRT; 308 AA.

Q9XFR7; AC; DT; 01-NOV-1999 (TREMBLrel. 12, Created)

DT; 01-NOV-1999 (TREMBLrel. 12, Last sequence update)

DT; 01-JUN-2003 (TREMBLrel. 24, Last annotation update)

DE; CRYCD4_1; GN; CYCD4_1; OS; Arabidopsis thaliana (Mouse-ear cress).

RA; Eukaryota; Viridiplantae; Streptophytina; Embryophytina; Tracheophytina; OC; Spermatophytina; Magnoliophytina; eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

OC; NCBI_TAXID=3702;

RN [1] - SEQUENCE FROM N.A.

RP de Veylder L., De Almeida Engler J., Bursens S., Manevski A.,

RA Lescure B., Van Montagu M., Engler G., Inze D.,

RT "A new D-type cyclin of Arabidopsis thaliana expressed during lateral

RT root primordia formation"; DR; Submitted (DRCI-1998) to the EMBL/GenBank/DBJ databases.

RL CC - SIMILARITY: BELONGS TO THE CYCLIN FAMILY.

DR EMBL; AU13636; CAB41347..1..

DR GO; GO:0005634; C:nucleus; IEA.

DR GO; GO:0000910; P:cytokinesis; IEA.

DR GO; GO:000074; P:regulation of cell cycle; IEA.

DR InterPro; IPR00570; Cyclin.

DR InterPro; IPR04367; Cyclin_Cterm.

DR InterPro; IPR00661; Cyclin_N.

DR PRAM; PR00134; cyclin; 1.

DR PRAM; PR02984; cyclin_C; 1.

DR SMART; SM00385; CYCLIN; 1.

DR PROSITE; SM00292; CYCLIN; 1.

17	10	3.2	355	10	Q9XAB7	Q7xab7 euphorbia e
18	9	2.9	371	10	Q84vB8	Q84vb8 populus alb
19	9	2.9	153	13	P79919	P79919 xenopus lae
20	9	2.9	198	10	Q8S521	Q8s521 zea mays (m
21	9	2.9	315	10	Q8GVE0	Q8gve0 helianthus
22	9	2.9	321	10	Q9SZ6	Q9sz6 arabidopsis
23	9	2.9	330	10	Q9SNV2	Q9snv2 antirrhinum
24	9	2.9	349	10	Q82678	Q82678 chenopodium
25	9	2.9	372	10	P93103	P93103 chenopodium
26	9	2.9	390	10	Q8S522	Q8s522 zea mays (m
27	8	2.6	178	5	Q23641	Q23641 caenorhabditis
28	8	2.6	232	17	Q9TB27	Q9tb27 thermoplasm
29	8	2.6	241	2	Q9ACH9	Q9ach9 uncultured
30	8	2.6	241	2	Q9ACT2	Q9act2 uncultured
31	8	2.6	241	2	Q9AE49	Q9ae49 uncultured
32	8	2.6	241	2	Q9AC10	Q9aci0 uncultured
33	8	2.6	241	2	Q9AC14	Q9aci4 uncultured
34	8	2.5	241	2	Q9AE47	Q9ae47 uncultured
35	8	2.5	241	2	Q9AC14	Q9aci4 uncultured
36	8	2.5	241	2	Q9ACH8	Q9ach8 uncultured
37	8	2.5	263	10	Q92156	Q92156 arabidopsis
38	8	2.6	300	17	Q28718	Q28718 archaeoglob
39	8	2.6	302	10	Q9E4G0	Q9e4g0 strongyloce
40	8	2.6	302	10	Q9E4G4	Q9e4g4 leishmania
41	8	2.6	308	10	Q8LPW3	Q8lpw3 helianthus
42	8	2.6	328	16	Q9HZ3	Q9hz3 pseudomonas
43	8	2.6	356	8	Q8LH8	Q8lh8 oryza sativ
44	8	2.6	357	10	Q8GVG9	Q8gvg9 helianthus

Query Match 100.0%; Score 308; DB 10; Length 308;

Best Local Similarity 100.0%; Pred. No. 1.7e-297; Indels 0; Gaps 0;

Matches 308; Conservative 0; Mismatches 0; Insertions 0; Deletions 0;

QY 1 MAEENLELSLICTESNVDEGMIWDETPIEISIPQMGFSOSEBEITMEMVEKEKQHUPS 60
 1 MAEENLELSLICTESNVDEGMIWDETPIEISIPQMGFSOSEBEITMEMVEKEKQHUPS 60
 Db 61 DDYIKRRLRGDDLDIINVGRDADLNWIKACEVHQGPLFCCLAMMYLDRFLSVHDLPSKG 120
 QY 61 DDYIKRRLRGDDLDIINVGRDADLNWIKACEVHQGPLFCCLAMMYLDRFLSVHDLPSKG 120
 Db 121 WIQLQAVACSLAAKIEETEVPMILDQVGDPOFVFEEAKSVORMELVINKWKIRAI 180
 QY 121 WIQLQAVACSLAAKIEETEVPMILDQVGDPOFVFEEAKSVORMELVINKWKIRAI 180
 Db 121 WIQLQAVACSLAAKIEETEVPMILDQVGDPOFVFEEAKSVORMELVINKWKIRAI 180
 QY 121 WIQLQAVACSLAAKIEETEVPMILDQVGDPOFVFEEAKSVORMELVINKWKIRAI 180
 Db 121 WIQLQAVACSLAAKIEETEVPMILDQVGDPOFVFEEAKSVORMELVINKWKIRAI 180
 QY 181 TPCSYIRFLRKMSKCDQEPSNTLISRSLQVIASTTKGIDLEFRPSE 228
 Db 181 TPCSYIRFLRKMSKCDQEPSNTLISRSLQVIASTTKGIDLEFRPSE 228
 QY 241 LQRHFDDNSFSPLSLLQKERVKKIGEMESDSDLCQTPNGYLEVSACCFSKTHS 300
 DB 241 LQRHFDDNSFSPLSLLQKERVKKIGEMESDSDLCQTPNGYLEVSACCFSKTHS 300
 QY 301 SSSYTHLS 308
 Db 301 SSSYTHLS 308

RESULT 2

Q9FKP7 PRELIMINARY; PRT; 308 AA.
 AC Q9FKP7;
 ID Q9FKP7; 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
 DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
 DB D-type cyclin.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; rosids;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Columbia;
 RX MEDLINE=9934145; PubMed=9679202;
 RA Kaneko T., Kotani H., Nakamura Y., Sato S., Asamizu E., Miyajima N.,
 RA Tabata S.;
 RT "Structural analysis of Arabidopsis thaliana chromosome 5. V. Sequence
 features of the regions of 1,381,565 bp covered by twenty one
 physically assigned pL and TAC clones.";
 RL DNA Res. 5:131-145(1998).
 CC - SIMILARITY: BELONGS TO THE CYCLIN FAMILY.
 DR Submitted (MAR-2002) to the EMBL/Genbank/DBJ databases.
 DR EMBL; AX084386; AAM60633.1; -
 DR GO; GO:0005634; C:nucleus; IEA.
 DR GO; GO:0000910; P:cyclotinensis; IEA.
 DR GO; GO:000074; P:regulation of cell cycle; IEA.
 DR InterPro; IPR006670; Cyclin.
 DR InterPro; IPR004367; Cyclin_Cterm.
 DR InterPro; IPR006671; Cyclin_N.
 DR Pfam; PF02984; cyclin; 1.
 DR Pfam; PF02984; cyclin_C; 1.
 DR SMART; SM00855; CYCLIN; 1.
 DR PROSITE; PS00292; CYCLINS; 1.
 DR Cell cycle; Cell division; Cyclin.
 KW SEQUENCE 308 AA; 34788 MN; EB077DA1B68DC42 CRC64;

Query Match. Best Local Similarity 55.5%; Score 171; DB 10; Length 308; Matches 171; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Query 1 MAEENLELSLICTESNVDEGMIWDETPIEISIPQMGFSOSEBEITMEMVEKEKQHUPS 60
 1 MAEENLELSLICTESNVDEGMIWDETPIEISIPQMGFSOSEBEITMEMVEKEKQHUPS 60
 Db 61 DDYIKRRLRGDDLDIINVGRDADLNWIKACEVHQGPLFCCLAMMYLDRFLSVHDLPSKG 120
 QY 61 DDYIKRRLRGDDLDIINVGRDADLNWIKACEVHQGPLFCCLAMMYLDRFLSVHDLPSKG 120
 Db 121 WIQLQAVACSLAAKIEETEVPMILDQVGDPOFVFEEAKSVORMELVINKWKIRAI 171
 QY 121 WIQLQAVACSLAAKIEETEVPMILDQVGDPOFVFEEAKSVORMELVINKWKIRAI 171

Query Match. Best Local Similarity 74.0%; Score 228; DB 10; Length 308; Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Query 1 MAEENLELSLICTESNVDEGMIWDETPIEISIPQMGFSOSEBEITMEMVEKEKQHUPS 60
 1 MAEENLELSLICTESNVDEGMIWDETPIEISIPQMGFSOSEBEITMEMVEKEKQHUPS 60
 Db 61 DDYIKRRLRGDDLDIINVGRDADLNWIKACEVHQGPLFCCLAMMYLDRFLSVHDLPSKG 120
 QY 61 DDYIKRRLRGDDLDIINVGRDADLNWIKACEVHQGPLFCCLAMMYLDRFLSVHDLPSKG 120

RESULT 4

Q9LK96 PRELIMINARY; PRT; 317 AA.

AC Q8LX96; DR Pfam; PF00134; cyclin; 1.
 DT 01-OCT-2000 (TREMBLrel. 15, Created) DR Pfam; PF02984; cyclin C; 1.
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update) DR SMART; SM00385; CYCLIN; 1.
 DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update) DR PROSITE; PS00292; CYCLINS; 1.
 DE Cyclin protein-like. KW Cell cycle; Cell division; Cyclin.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicots; rosids;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 OX NCBI_TaxID=3702;
 RN [1] SEQUENCE FROM N.A.
 RP Bevan M., Bancroft I., Mewes H.W., Rudd S., Lemcke K., Mayer K.F.X.;
 RL Submitted (AER-2000) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RA EU Arabidopsis sequencing project;
 RL Submitted (AER-2000) to the EMBL/GenBank/DBJ databases.
 CC -!- SIMILARITY: BELONGS TO THE CYCLIN FAMILY.
 DR EMBL; AL353995; CB89399.1; -.
 DR PIR; T49995; T49995.
 DR GO; GO:005634; C:nucleus; IEA.
 DR GO; GO:000910; P:cytokinesis; IEA.
 DR GO; GO:000074; P:regulation of cell cycle; IEA.
 DR InterPro; IPR006670; Cyclin.
 DR InterPro; IPR004367; Cyclin_Cterm.
 DR Pfam; PP00134; cyclin; 1.
 DR Pfam; PP02984; cyclin_C; 1.
 DR PROSITE; PS00292; CYCLINS; 1.
 DR Cell cycle; Cell division; Cyclin.
 KW Sequence 317 AA; 35910 MW; 07616F948092771 CRC64;
 SQ

Query Match 6.5%; Score 20; DB 10; Length 317;
 Best Local Similarity 100.0%; Pred. No. 4.2e-11; Indels 0; Gaps 0;
 Matches 20; Conservative 0; Mismatches 0; RT
 QY 100 CLAMMYLDPLSVDLPSK 119
 Db 91 CLAMMYLDPLSVDLPSK 110

RESULT 5

Q8RX9 PRELIMINARY; PRT; 354 AA.

RT

Q8RX9 PRELIMINARY; PRT; 354 AA.

AC Q8RX9; DR Pfam; PF00134; cyclin; 1.
 DT 01-MAY-1999 (TREMBLrel. 10, Created) DR SMART; SM00385; CYCLIN; 1.
 DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update) DR PROSITE; PS00292; CYCLINS; 1.
 DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update) DR InterPro; IPR004367; Cyclin_Cterm.
 DE Cyclin D2.1 protein. KW CYCD2.1
 OS Nicotiana tabacum (Common tobacco).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicots; asterids;
 OC Lamiales; Solanales; Solanaceae; Nicotiana.
 RN [1] SEQUENCE FROM N.A.
 RP SEQUENCE FROM N.A.
 RX MEDLINE-9909070; PUBMED=9810377;
 RA Sorrell D.A., Combettes B., Chaubet-Gigot N., Gigot C., Murray J.A.H.;
 RT "Distinct Cyclin D Genes Show Mitotic Accumulation or Constant Levels
 RT of Transcripts in Tobacco Bright Yellow-2 Cells";
 RL Plant Physiol. 119:343-351(1999).
 CC ! SIMILARITY: BELONGS TO THE CYCLIN FAMILY.
 DR EMBL; AD01182; CA09822.1; -.
 DR GO; GO:0005634; C:nucleus; IEA.
 DR GO; GO:000910; P:cytokinesis; IEA.
 DR GO; GO:000074; P:regulation of cell cycle; IEA.
 DR InterPro; IPR006670; Cyclin.
 DR InterPro; IPR004367; Cyclin_Cterm.
 DR InterPro; IPR006671; Cyclin_N.
 DR Pfam; PP00134; cyclin; 1.
 DR PROSITE; PS00292; CYCLINS; 1.
 DR Cell cycle; Cell division; Cyclin.
 KW Sequence 356 AA; 38937 MW; 502AF4EB9CB8BCEA CRC64;

Query Match 4.2%; Score 13; DB 10; Length 356;
 Best Local Similarity 100.0%; Pred. No. 0.0042; Indels 0; Gaps 0;
 Matches 13; Conservative 0; Mismatches 0; RT
 QY 124 QLLAVACISLAAK 136
 Db 149 QLLAVACISLAAK 161

RESULT 7

Q8L6U0 PRELIMINARY; PRT; 382 AA.

RT

Q8L6U0 PRELIMINARY; PRT; 382 AA.

AC Q8L6U0; DR Pfam; PF00134; cyclin; 1.
 DT 01-OCT-2002 (TREMBLrel. 22, Created) DR SMART; SM00385; CYCLIN; 1.
 DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update) DR PROSITE; PS00292; CYCLINS; 1.
 DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update) DR CYCD2.
 DE CYCD2; DR
 OS Daucus carota (Carrot).

OC
OC
OC
OC
OC
OC
RN
RP
SEQUENCE FROM N.A.
RA
Eun C.H., Ko S.M., Matsubayashi Y., Sakagami Y., Kamada H.;
RT
"The effect of the peptidyl growth factor, phytosuifokine-alpha, on
the cell cycle progression in carrot non-embryogenic cells."
RL
Submitted (URL=) to the EMBL/GenBank/DBJ databases.
CC
-1- SIMILARITY: BELONGS TO THE CYCLIN FAMILY.
DR
EMBL; AA496740; CRC4141.1; --.
DR
GO; GO:000534; C:nucleus; IEA.
DR
GO; GO:0000310; P:cytokinesis; IEA.
DR
InterPro; IPR00074; P:regulation of cell cycle; IEA.
DR
InterPro; IPR004367; Cyclin_Cterm.
DR
InterPro; IPR006671; Cyclin_N.
DR
Pfam; PF00134; cyclin; 1.
DR
SMART; SN00365; CYCLIN; 1.
DR
PROSITE; PS00292; CYCLINS; 1.
KW
Cell cycle; Cell division; Cyclin.
SEQUENCE 382 AA; 43354 MW; 797F88528DB09170 CRC64;

Query Match 4.2%; Score 13; DB 10; Length 382;
Best Local Similarity 100.0%; Pred. No. 0.00045; Mismatches 0; Indels 0; Gaps 0;
Matches 13; Conservative 0; SMART; SM00365; CYCLIN; 1.

QY 124 QLIAVACSLAAK 136
Db 141 QLIAVACSLAAK 153

RESULT 8
Q8AVQ4 PRELIMINARY; PRT; 291 AA.
ID Q8AVQ4
AC
DT 01-MAR-2003 (TREMBrel. 23, Created)
DT 01-OCT-2003 (TREMBrel. 25, Last annotation update)
DE Similar to cyclin D1 (PRAD; parathyroid adenomatosis 1).
OS Xenopus laevis (African clawed frog).
OC
Amphibia; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Ripoidea; Pipidae;
OC Xeropoda; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
SEQUENCE FROM N.A.
RC
TISSUE=Embryo;
RA Klein S., Straubberg R.;
RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
DR
EMBL; BB041525; AAH41525.1; --.
DR
GO; GO:000534; C:nucleus; IEA.
DR
GO; GO:0000310; P:regulation of cell cycle; IEA.
DR
InterPro; IPR006670; Cyclin.
DR
InterPro; IPR004367; Cyclin_Cterm.
DR
Pfam; PF00134; cyclin; 1.
DR
SMART; SM00365; CYCLIN; 1.
DR
PROSITE; PS00292; CYCLIN; 1.
DR
Hypothetical protein.
KW
SEQUENCE 291 AA; 33005 MW; 667BC2C9EACF9178 CRC64;

Query Match 3.9%; Score 12; DB 13; Length 291;
Best Local Similarity 100.0%; Pred. No. 0.0035; Mismatches 0; Indels 0; Gaps 0;
Matches 12; Conservative 0; SMART; SM00365; CYCLIN; 1.

QY 101 LAMNYLDRLFSV 112
Db 78 LAMNYLDRLFSV 89

RESULT 10
Q8OPP4 PRELIMINARY; PRT; 291 AA.
ID Q8OPP4
AC
DR
DT 01-JUN-2002 (TREMBrel. 21, Created)
DT 01-JUN-2002 (TREMBrel. 24, Last annotation update)
DE Cyclin D1.
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
SEQUENCE FROM N.A.
RC
TISSUE=Mature ovary;
RA Bauer M.P., Goetz F.W.;
RT "Isolation of Cyclin D1 from the Zebrafish.";
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ database_B.
CC
-1- SIMILARITY: BELONGS TO THE CYCLIN FAMILY.
DR
EMBL; AA365847; RAM0355.1; --.
DR
GO; GO:000534; C:nucleus; IEA.
DR
GO; GO:0000910; P:cytokinesis; IEA.
DR
GO; GO:0000074; P:regulation of cell cycle; IEA.
DR
InterPro; IPR006670; Cyclin.
DR
InterPro; IPR004367; Cyclin_Cterm.
DR
InterPro; IPR006671; Cyclin_N.
DR
InterPro; IPR001092; HLH_basic.

Query Match 3.9%; Score 12; DB 13; Length 291;
Best Local Similarity 100.0%; Pred. No. 0.0035; Mismatches 0; Indels 0; Gaps 0;
Matches 12; Conservative 0; SMART; SM00365; CYCLIN; 1.

QY 101 LAMNYLDRLFSV 112
Db 78 LAMNYLDRLFSV 89

DR	Pfam; PF00134; cyclin; 1.
DR	PFAM; PF02384; cyclin_C; 1.
DR	SMART; SM00385; CYCLIN; 1.
DR	PROSITE; PS00292; CYCLINS; 1.
KW	Cell cycle; Cell division; Cyclin.
SQ	SEQUENCE 291 AA; 33080 MW; 784EBFCF2482EE8 CRC64;
Query Match	3.9%; Score 12; DB 13; Length 291;
Best Local Similarity	100.0%; Pred. No. 0.0035; Indels 0; Gaps 0;
Matches	12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	101 LANNYDPLFSV 112
DB	80 LANNYDRELPSV 91
RESULT 11	
ID	Q99NB4 PRELIMINARY; PRT; 191 AA.
AC	Q99NB4; 01-JUN-2001 (TREMBLrel. 17, Created)
DT	01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DR	01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE	Cyclin D1 (Fragment).
OS	Rattus norvegicus (Rat).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;	[1]
RN	SEQUENCE FROM N.A.
RC	STRAIN=Wistar; RA
RA	Moriochi A., Ido A., Tsubouchi H.; "Characterization of rat cyclin D1 5' flanking region."; Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.
RL	-!- SIMILARITY: BELONGS TO THE CYCLIN FAMILY.
DR	EMBL; AB02564; BAB40333.1; -. HSSP; P30274; IWIN.
DR	GO; GO:0005634; C:nucleus; IEA.
DR	GO; GO:000910; P:cyclokinase; IEA.
DR	GO; GO:0000074; P:regulation of cell cycle; IEA.
DR	InterPro; IPR006670; Cyclin.
DR	InterPro; IPR004367; Cyclin_Cterm.
DR	InterPro; IPR006671; Cyclin_N.
DR	IntePro; IPR001092; HLH_basic.
DR	Pfam; PF00134; cyclin; 1.
DR	PFAM; PF02384; CYCLIN; 1.
DR	SMART; SM00385; CYCLINS; 1.
DR	PROSITE; PS00292; CYCLINS; 1.
DR	PROSITE; PS00038; HLH 1; 1.
DR	PROSITE; PS00038; HLH 1; 1.
DR	PROSITE; PS00038; HLH 1; 1.
DR	PROSITE; PS00038; HLH 1; 1.
DR	PROSITE; PS00038; HLH 1; 1.
FT	cell cycle; Cell division; Cyclin.
FT	NON_TER 191 191
SO	SEQUENCE 191 AA; 22203 MW; AA97B6E0F332EDEE CRC64;
Query Match	3.6%; Score 11; DB 11; Length 191;
Best Local Similarity	100.0%; Pred. No. 0.024; Mismatches 0; Indels 0; Gaps 0;
Matches	11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	101 LANNYDPLFSV 111
DB	80 LANNYDPLFLS 90
RESULT 12	
DR	Pfam; PF00134; cyclin; 1.
DR	PFAM; PF02384; cyclin_C; 1.
DR	SMART; SM00385; CYCLIN; 1.
DR	PROSITE; PS00292; CYCLINS; 1.
KW	Cell cycle; Cell division; Cyclin.
SQ	SEQUENCE 291 AA; 33080 MW; 784EBFCF2482EE8 CRC64;
Query Match	3.9%; Score 12; DB 13; Length 291;
Best Local Similarity	100.0%; Pred. No. 0.0035; Indels 0; Gaps 0;
Matches	12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	101 LANNYDPLFSV 112
DB	80 LANNYDRELPSV 91
RESULT 13	
ID	Q98BL9 PRELIMINARY; PRT; 156 AA.
AC	Q98BL9; 01-JUN-2001 (TREMBLrel. 17, Created)
DT	01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DR	01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE	Cyclin D2.
GN	CCND2.
OS	Mus musculus (Mouse).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;	[1]
RN	SEQUENCE FROM N.A.
RC	STRAIN=C57BL/6J; TISSUE=Pancreas;
RC	MEIDINE-2108660; PubMed=12171851;
RA	Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y., Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S., Kadota K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamakawa I., Saito T., Oizaki Y., Gojobori T., Bono H., Kanukawa T., Saito R., Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H., Kuehl P., Lewis S., Matsuo Y., Nikaido I.I., Pesole G., Quackenbush J., Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T., Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G., Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F., Brownstein M.J., Bult C., Fletcher C., Fujita M., Garibaldi M., Guettinrich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H., Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P., Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., Sakai H., Sato K., Schoenbach C., Seiya T., Shibata Y., Storch K.-F., Suzuki H., Toyo-oka K., Wang K.H., Wetz C., Whittaker C., Wilming L., Wysshaek-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsuki S., Hayashizaki Y.;
RT	"Functional annotation of a full-length mouse cDNA collection.";
RL	NCBI 409:695-696(2001);
CC	-!- SIMILARITY: BELONGS TO THE CYCLIN FAMILY.
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophytta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC	PACCAD clade; Panicoideae; Andropogoneae; Zea; Zea; NCBI_TaxID=4577;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	STRAIN=CV. Mol17;
RA	Tao Y., Lowe K., Gregory C., Coughlan S.J., Gordon-Kamm W.J.; "Isolation of a family of D-type cyclins from maize that show conserved and unique characteristics.";
RT	Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
RL	-!- SIMILARITY: BELONGS TO THE CYCLIN FAMILY.
CC	EMBL; AB351189; ALA18956.1; -.
DR	GO; GO:0005634; C:nucleus; IEA.
DR	GO; GO:000910; P:cyclokinase; IEA.
DR	GO; GO:000074; P:regulation of cell cycle; IEA.
DR	InterPro; IPR006670; Cyclin.
DR	InterPro; IPR004367; Cyclin_Cterm.
DR	InterPro; IPR006671; Cyclin_N.
DR	Pfam; PF00114; cyclin; 1.
DR	PFAM; PF02984; cyclin_C; 1.
DR	SMART; SM00385; CYCLIN; 1.
DR	PROSITE; PS00292; CYCLINS; 1.
KW	Cell cycle; Cell division; Cyclin.
SQ	SEQUENCE 358 AA; 38336 MW; D25B39DB7D640837 CRC64;
Query Match	3.6%; Score 11; DB 10; Length 358;
Best Local Similarity	100.0%; Pred. No. 0.041; Mismatches 0; Indels 0; Gaps 0;
Matches	11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	124 QLLAVACSLIA 134
DB	148 QLLAVACSLIA 158
RESULT 14	
ID	Q98BL9 PRELIMINARY; PRT; 156 AA.
AC	Q98BL9; 01-JUN-2001 (TREMBLrel. 17, Created)
DT	01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DR	Cyclin D2.
GN	CCND2.
OS	Mus musculus (Mouse).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;	[1]
RN	SEQUENCE FROM N.A.
RC	STRAIN=C57BL/6J; TISSUE=Pancreas;
RC	MEIDINE-2108660; PubMed=12171851;
RA	Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y., Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S., Kadota K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamakawa I., Saito T., Oizaki Y., Gojobori T., Bono H., Kanukawa T., Saito R., Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H., Kuehl P., Lewis S., Matsuo Y., Nikaido I.I., Pesole G., Quackenbush J., Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T., Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G., Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F., Brownstein M.J., Bult C., Fletcher C., Fujita M., Garibaldi M., Guettinrich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H., Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P., Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., Sakai H., Sato K., Schoenbach C., Seiya T., Shibata Y., Storch K.-F., Suzuki H., Toyo-oka K., Wang K.H., Wetz C., Whittaker C., Wilming L., Wysshaek-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsuki S., Hayashizaki Y.;
RT	"Functional annotation of a full-length mouse cDNA collection.";
RL	NCBI 409:695-696(2001);
CC	-!- SIMILARITY: BELONGS TO THE CYCLIN FAMILY.

DR	EMBL; A007904; BAB25338.1; -.	DT	01-MAY-2000 (TREMBLrel. 13, last sequence update)
DR	HSSP; P3524; IVIN.	DT	01-JUN-2003 (TREMBLrel. 24, last annotation update)
DR	MCD; MGI:83314; Ccd2.	DE	Cyclin D3a (Fragment).
DR	GO; GO:000077; Regulation of cell cycle; IMP.	GN	Antirrhinum majus (Garden snapdragon).
DR	InterPro; IPR006670; Cyclin.	OS	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
DR	InterPro; IPR006671; Cyclin_N.	OC	Spermatophyta; Magnoliopsida; eudicotyledons; core eudicots; asterids;
DR	Pfam; PF0134; cyclin_1.	OC	Lamiales; Plantaginaceae; Antirrhineae; Antirrhinum.
DR	SMART; SM00385; CYCLINS; 1.	OK	NCBI_TaxID=4151;
DR	PROSITE; PS00292; CYCLINS; 1.	RN	[1]
KW	Cell cycle; Cell division; Cyclin.	RP	SEQUENCE FROM N.A.
SQ	Query Match 3.2%; Score 10; DB 11; Length 156; Best Local Similarity 100.0%; Pred. No. 0.2; Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	RA	Gaudin V., Jumess P., Robert P., Towers M., Riou-Khamlichi C., Murray J., Coen E., Doonan J.H.; "The expression of D-cyclin genes define distinct developmental zones in Antirrhinum apical meristems and is locally regulated by the cycloidea gene."
Db	101 LAMNYDLRFL 110 78 LAMNYDLRFL 87	RT	Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.
RESULT 14		RL	- SIMILARITY: BELONGS TO THE CYCLIN FAMILY.
O57481	PRELIMINARY; PRT; 190 AA.	DR	EMBL; AJ250397; CAB61222.1; -.
ID	O57481: 01-JUN-1998 (TREMBLrel. 06, Created)	DR	GO; GO:0005634; C:nucleus; IEA.
AC	DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)	DR	GO; GO:000074; P:regulation of cell cycle; IEA.
AC	DT 01-JUN-1998 (TREMBLrel. 24, Last annotation update)	DR	InterPro; IPR006670; Cyclin.
DE	Cyclin D (Fragment).	DR	InterPro; IPR006671; Cyclin_N.
OS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Buteleosteii; Neoteleostei; Acanthomorpha; Acanthopterygii; Percormorpha; Perciformes; Percoidae; Stizostedion.	DR	Pfam; PF00334; cyclin_1.
OC	NCBI_TaxID=57868; [1]	DR	SMART; SM00385; CYCLIN; 1.
OC	SEQUENCE FROM N.A.	DR	PROSITE; PS00292; CYCLINS; 1.
RP	MEDLINE=98440539; PubMed=9765420; Lapierre L.A., Casey J.W., Holzschu D.L.; "Walleye retroviruses associated with skin tumors and hyperplasias encode cyclin D homologs."	KW	Cell cycle; Cell division; Cyclin.
RA	J. Virol. 72:8765-8771(1998).	FT	NON_TER 343 343 AA; 39254 MW; 128210AB2FC6E2C6 CRC64;
RT	CC -1- SIMILARITY: BELONGS TO THE CYCLIN FAMILY.	SQ	SEQUENCE 343 AA; 39254 MW; 128210AB2FC6E2C6 CRC64;
RT	DR HSSP; P30274; IVIN.	Query Match 3.2%; Score 10; DB 10; Length 343; Best Local Similarity 100.0%; Pred. No. 0.39; Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
RT	DR GO; GO:0005634; C:nucleus; IEA.	Db	127 AVACSLAAK 136 136 AVACSLAAK 145
RT	DR GO; GO:0000910; :cytokinesis; IEA.	Search completed: March 23, 2004, 16:48:14	Job time : 65 secs
RT	DR GO; GO:0000074; P:regulation of cell cycle; IEA.		
RL	DR InterPro; IPR006670; Cyclin.		
RL	DR InterPro; IPR003367; Cyclin_Cterm.		
RL	DR InterPro; IPR006671; Cyclin_N.		
RL	DR Pfam; PF00134; cyclin; 1.		
RL	DR Pfam; PF02984; cyclin_C; 1.		
RL	DR SMART; SM00385; CYCLIN; 1.		
CC	Cell cycle; Cell division; Cyclin.		
CC	NON_TER 1 1		
CC	FT 190 190 AA; 21445 MW; 5EB1B9BA969C01BC CRC64;		
CC	FT NON_TER 190 190 AA; 21445 MW; 5EB1B9BA969C01BC CRC64;		
RESULT 15			
O9SNV1	PRELIMINARY; PRT; 343 AA.		
ID	O9SNV1		
AC	O9SNV1; 01-MAY-2000 (TREMBLrel. 13, Created)		
AC	Match 3.2%; Score 10; DB 13; Length 190; Best Local Similarity 100.0%; Pred. No. 0.24; Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
QY	101 LAMNYDLRFL 110 18 LAMNYDLRFL 27		
Db			